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(54) Title: METHOD FOR DETECTION OF NUCLEIC ACID TARGET SEQUENCES INVOLVING IN VITRO TRANSCRIPTION FROM AN RNA PROMOTER			
(57) Abstract			
<p>Disclosed is a method of detecting the presence of a nucleic acid target sequence of interest, the method comprising the steps of: (a) adding first and second nucleic acid probes to a sample comprising the sequence of interest, so as to form a complex comprising three strands of nucleic acid, wherein the first probe comprises the full length sequence of a first strand of a double stranded promoter, the target sequence comprises an end part of a second strand of the double stranded promoter which is complementary to a part of the first strand, and the second probe comprises the rest of the second strand of the double stranded promoter which is complementary to a part of the first strand, such that a functional promoter is formed when the first probe is hybridised to both the target sequence and to the second probe; (b) adding a polymerase which recognises the promoter, so as to cause the <i>de novo</i> synthesis of nucleic acid from the promoter present in the complex; and (c) detecting directly or indirectly the <i>de novo</i> synthesised nucleic acid. Also disclosed is the complex formed in performance of the method defined above, and a kit for performing the method defined above.</p>			

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METHOD FOR DETECTION OF NUCLEIC ACID TARGET SEQUENCES INVOLVING IN VITRO TRANSCRIPTION FROM AN RNA PROMOTER

Field of the Invention

The present invention relates to nucleic acid hybridisation probes and complexes formed therefrom, their use in nucleic acid amplification and/or nucleic acid detection processes and to kits comprising the probes and for forming said complexes. The present invention is particularly concerned with transcription and amplification of hybridised nucleic acid probes such that sensitivity of hybridisation reactions is increased.

Background of the Invention

All publications mentioned in this specification are incorporated herein by reference.

Much research has been carried out on RNA polymerases, especially bacteriophage RNA polymerases. Generally, bacteriophage RNA polymerases are exceptionally active for *in vitro* transcription. This high level activity may be due in part to the fact that they are composed of a single polypeptide chain and do not require a dissociating initiation factor. These polymerases have been shown to be more active on supercoiled templates although they are also very active on linear templates (Smeekens & Romano 1986 Nucl. Acids Res. 14, 2811).

Specifically, the RNA polymerase from the bacteriophage T7 has been shown to be very selective for specific promoters that are rarely encountered in DNA unrelated to T7 DNA (Chamberlin *et al.*, 1970 Nature 228, 227; Dunn & Studier 1983 J. Mol. Biol. 166, 477). T7 RNA polymerase is able to make complete transcripts of almost any DNA that is placed under control of a T7 promoter. T7 RNA polymerase is a highly active enzyme that transcribes about five times faster than does *Escherichia coli* RNA polymerase (Studier *et al.*, 1990 Methods Enzymol. 185, 60). The synthesis of small RNAs using T7 RNA polymerase has been described whereby sequences around the RNA polymerase promoter sequence are shown to be important in the reproducible improvement of yield of RNA produced (Milligan & Uhlenbeck, 1989 Methods Enzymol. 180, 51 and Milligan *et al.*, 1987 Nucl. Acids Res. 15, 8783-8798). Other RNA polymerases that have similar

properties to T7 include those from bacteriophage T3 and SP6, the genes for which have all been cloned and the corresponding enzymes are commercially available.

A number of nucleic acid amplification processes are disclosed in the prior art. One such process is polymerase chain reaction (PCR) disclosed in US 4683195 and 4683202. The PCR amplification process is very well-known and successful. However PCR does have drawbacks including the need for adjusting reaction temperatures alternately between intermediate (e.g. 50°C-55°C) and high (e.g. 90°C-95°C) temperatures involving repeated thermal cycling. Also, the time scale required for multiple cycles of large temperature transitions to achieve amplification of a nucleic acid sequence and the occurrence of sequence errors in the amplified copies of the nucleic acid sequence is a major disadvantage as errors occur during multiple copying of long sequence tracts. Additionally, detection of the amplified nucleic acid sequence generally requires further processes e.g. agarose gel electrophoresis.

Alternative nucleic acid amplification processes that do utilize RNA polymerases are disclosed in WO 88/10315 (Siska Diagnostics), EP 329822 (Cangene) EP 373960 (Siska Diagnostics), US 5,554,516 (Gen-Probe Inc.), WO 89/01050 (Burg *et al*), WO 88/10315 (Gingeras *et al*), and EP 329822 (Organon Teknika), which latter document relates to a technique known as NASBA. These amplification processes describe a cycling reaction comprising of alternate DNA and RNA synthesis. This alternate RNA/DNA synthesis is achieved principally through the annealing of oligonucleotides adjacent to a specific DNA sequence whereby these oligonucleotides comprise a transcriptional promoter. The RNA copies of the specific sequence so produced, or alternatively an input sample comprising a specific RNA sequence (US 5,554,516), are then copied as DNA strands using a nucleic acid primer and the RNA from the resulting DNA:RNA hybrid is either removed by denaturation (WO 88/10315) or removed with RNase H (EP 329822, EP 373960 & US 5,554,516).

The annealing of oligonucleotides forming a transcription promoter is then repeated in order to amplify RNA production. Amplification is thus achieved principally through the use of efficient RNA polymerases to produce an excess of RNA copies over DNA

templates. The RNase version of this method has great advantages over PCR in that amplification can potentially be achieved at a single temperature (i.e. isothermally). Additionally, a much greater level of amplification per cycle can be achieved than for PCR i.e. a doubling of DNA copies per cycle for PCR; 10-100 RNA copies per cycle using T7 RNA polymerase.

The processes described above all refer to methods whereby a specific nucleic acid region is directly copied and these nucleic acid copies are further copied to achieve amplification. The variability between various nucleic acid sequences is such that the rates of amplification between different sequences by the same process are likely to differ, thus presenting problems for example in the quantitation of the original amount of specific nucleic acid.

The processes listed above have a number of disadvantages in the amplification of their target nucleic acid; therefore, a list of desiderata for the sensitive detection of a specific target nucleic acid sequence is outlined below;

- a) the process should preferably not require copying of the target sequence,
- b) the process should preferably not involve multiple copying of long tracts of sequence,
- c) the process should preferably be generally applicable to both DNA and RNA target sequences including specific sequences without discrete ends,
- d) the signal should preferably result from the independent hybridisation of two different probes, or regions of probe, to a target sequence,
- e) the process should preferably include an option for detection of hybridised probe without any additional steps.

A nucleic acid amplification process that fulfils the above desiderata is disclosed in WO 93/06240 (Cytocell Ltd). Two amplification processes are described, one thermal and one isothermal. Both the thermal and isothermal versions depend on the hybridisation of two nucleic acid probes of which regions are complementary to the target nucleic acid. Portions of said probes being capable of hybridising to the sequence of interest such that the probes are adjacent or substantially adjacent to one another, so as to enable complementary arm specific sequences of the first and second probes to become annealed

to each other. Following annealing, chain extension of one of the probes is achieved by using part of the other probe as a template. Amplification of the extended probe is achieved by one of two means; in the thermal cycling version thermal separation of the extended first probe is carried out to allow hybridisation of a further probe, substantially complementary to part of the newly synthesised sequence of the extended first probe. Extension of the further probe by use of an appropriate polymerase using the extended first probe as a template is achieved. Thermal separation of the extended first and further probe products provides templates for the extension of further first probe molecules and the extended first probe can act as a template for the extension of other further probe molecules.

In the isothermal version, primer extension of the first probe creates a functional RNA polymerase promoter that in the presence of a relevant RNA polymerase, allows for transcription of the probe sequence producing multiple copies of RNA. The resulting RNA is further amplified as a result of the interaction of complementary DNA oligonucleotides containing further RNA polymerase promoter sequences, whereupon annealing and extension of the RNA on the DNA oligonucleotide leads to a further round of RNA. This cyclical process generates large yields of RNA, detection of which can be achieved by a number of means.

Summary of the Invention

In a first aspect the invention provides a complex comprising three strands of nucleic acid: a promoter strand, a promoter complementary strand, and a target strand; wherein the promoter complementary strand comprises the full length sequence of a first strand of a double stranded promoter; the target strand comprises a part of a second strand of the double stranded promoter; and the promoter strand comprises a part of the second strand of the double stranded promoter which is complementary to a part of the first strand; wherein neither part of the second strand of the double stranded promoter present on the target strand or on the promoter strand is capable of forming a substantially functional promoter when hybridised to the promoter complementary strand in the absence of the other part, but wherein a substantially functional promoter is formed when the promoter complementary strand is hybridised to both the target strand and the promoter strand.

The promoter strand ("PS") and the promoter complementary strand ("CS") are conveniently provided as a pair of respective "PS" and "CS" nucleic acid probes. The probes may comprise DNA, peptide nucleic acid (PNA), locked nucleic acid (LNA), (less preferably RNA) or any combination thereof.

PNA is a synthetic nucleic acid analogue in which the sugar/phosphate backbone is replaced by a peptide-linked chain (typically of repeated N-(2-aminoethyl)-glycine units), to which the bases are joined by methylene carbonyl linkages. PNA/DNA hybrids have high T_m values compared to double stranded DNA molecules, since in DNA the highly negatively-charged phosphate backbone causes electrostatic repulsion between the respective strands, whilst the backbone of PNA is uncharged. Another characteristic of PNA is that a single base mis-match is, relatively speaking, more destabilizing than a single base mis-match in heteroduplex DNA. Accordingly, PNA is useful to include in probes for use in the present invention, as the resulting probes have greater specificity than probes consisting entirely of DNA. Synthesis and uses of PNA have been disclosed by, for example, Orum *et al*, (1993 Nucl. Acids Res. 21, 5332); Egholm *et al*, (1992 J. Am. Chem. Soc. 114, 1895); and Egholm *et al*, (1993 Nature 365, 566).

LNA is a synthetic nucleic acid analogue, incorporating "internally bridged" nucleoside analogues. Synthesis of LNA, and properties thereof, have been described by a number of authors: Nielsen *et al*, (1997 J. Chem. Soc. Perkin Trans. 1, 3423); Koshkin *et al*, (1998 Tetrahedron Letters 39, 4381); Singh & Wengel (1998 Chem. Commun. 1247); and Singh *et al*, (1998 Chem. Commun. 455). As with PNA, LNA exhibits greater thermal stability when paired with DNA, than do conventional DNA/DNA heteroduplexes. However, LNA can be synthesised on conventional nucleic acid synthesising machines, whereas PNA cannot. Therefore, in some respects, LNA is to be preferred over PNA, for use in probes in accordance with the present invention.

The substantially functional promoter created by the formation of the complex of the invention is an RNA promoter (i.e. a structure recognised by an RNA polymerase and which causes the synthesis of RNA in the presence of a suitable polymerase and reagents). A "substantially functional" promoter may be defined for present purposes as a nucleic

acid complex which possesses at least 20% or more (preferably at least 50%, more preferably at least 75%, and most preferably at least 90%) of the promoter activity of a fully double stranded, wild type promoter sequence, the relative amount of promoter activity being measured by quantitation of the amount of a given RNA transcript produced by the promoter in a given amount of time, under equivalent conditions (e.g. of temperature and ribonucleotide triphosphate concentration).

The target strand may comprise any nucleic acid (RNA or, more preferably DNA) sequence of interest, such as a sequence from a pathogen (such that the complex may be used to detect the presence of a pathogen), or may be the sequence of a particular human, animal or plant allele, such that the genotype of an individual human or animal may be determined. Conveniently (but not necessarily) at least that portion (typically 2-4 bases) of the target which contains the part of the second strand of the double stranded promoter will preferably comprise DNA. The target strand may comprise both DNA and/or RNA.

In a second aspect the invention provides a method of detecting the presence of a nucleic acid target sequence of interest, the method comprising: adding first and second probes to a sample comprising the sequence of interest, so as to form the complex of the first aspect of the invention; causing the synthesis of newly-synthesised ribonucleic acid from the substantially functional promoter present in the complex; and detecting directly or indirectly the newly-synthesised nucleic acid. The method may be used qualitatively or quantitatively. In particular, the method of the invention (and kits, as defined below) may be used for detecting the presence of single nucleotide polymorphisms ("SNP"s) in the target sequence, and may be used in high throughput screening (HTS) for pharmacogenomic investigations.

In a third aspect the invention provides a kit for forming the complex of the first aspect of the invention, the kit comprising a pair of probe molecules corresponding to the promoter strand and the promoter complementary strand, and appropriate packaging means. The kit will preferably be suitable for performing the method of the second aspect of the invention. The kit will therefore optionally comprise one or more of the following components: an RNA polymerase (particularly a T3, T7 or SP6 RNA polymerase), a DNA

polymerase (particularly Klenow fragment of DNA polymerase I, ϕ 29 polymerase, *Bst* polymerase and SequenaseTM), deoxyribonucleotide or ribonucleotide triphosphates (labelled or unlabelled), labelling reagents and/or detection reagents (e.g. fluorophores), buffers, and instructions for use according to the method of the second aspect of the invention.

Thus, typically, the nucleic acid complex of the invention will comprise a target sequence, a CS probe, and a PS probe. The CS probe (bearing the "promoter complementary strand") comprises a target-specific region (or "foot") which hybridises specifically to the target sequence. This target-specific region comprises the first few bases (preferably the first 2-4 bases, most preferably the first three bases) of an RNA polymerase promoter, which are hybridised with complementary bases in the target sequence. This "foot" region of the CS probe may conveniently comprise LNA and/or PNA, which increases the specificity of hybridisation. Where PNA is used, all or nearly all of the target complementary region may comprise PNA. If LNA is used, it will normally suffice for 2-5 bases of the target-complementary portion to comprise LNA, the rest typically comprising conventional nucleic acid. The CS probe also comprises a non target-complementary "arm" region, which is adjacent to and contiguous with the target-specific foot region and which comprises the rest of the RNA polymerase promoter sequence.

The PS probe (bearing the "promoter strand") comprises a portion that is complementary to the "arm" region of the CS probe. The PS probe provides the rest of the sequence required to form a substantially functional RNA polymerase promoter. If desired, the PS probe may additionally comprise a target-specific "foot" region which hybridises to the target strand in a position substantially adjacent to the CS probe, but the presence of such a target-specific region in the PS probe is not essential for performance of the invention. Where the PS probe comprises a target-complementary "foot", the foot may comprise PNA and/or LNA, as described above.

The PS probe preferably comprises a 5' template portion, which is transcribed into multiple RNA copies upon formation of the functional RNA polymerase promoter. The general principle of the invention is illustrated in Figures 1 and 2, and described in greater

detail below. The arrangement is such that, in the absence of target nucleic acid, substantially no *de novo* RNA is synthesized, as no substantially functional RNA promoter is formed (the probes hybridised together, in the absence of target, being unable to provide at least 20% of the activity of the fully double stranded wild type promoter).

The present inventors are the first to appreciate that one of the strands of a double stranded RNA promoter may be discontinuous, and formed by non-ligated separate nucleic acid molecules, and yet still provide a substantially functional RNA promoter. More particularly, the inventors are the first to appreciate that this phenomenon can be utilised to provide a method of detecting the presence and/or amount of a nucleic acid sequence of interest.

The RNA polymerase promoter is preferably one recognised by a bacteriophage RNA polymerase, for example, T3, T7 or SP6 polymerase or any of the mutant forms thereof which are known to those skilled in the art. Particular mutant RNA polymerases which may be useful in performing the method of the invention are known, which may synthesise RNA or DNA (see Kostyuk *et al*, 1995 FEBS Letts. 369, 165-168).

The sequence of the T3 RNA polymerase promoter (described in the prior art) is:

5' AAATTAACCCTCACTAAA 3'
3' TTTAATTGGGAGTGATTT 5' (Seq. ID Nos. 1 and 2)

(A number of variant T3 promoter sequences are also known, especially those in which the first three bases of the non-template strand [the upper strand shown above] are 5' TTA 3', rather than AAA.)

The sequence of the T7 RNA polymerase promoter (described in the prior art) is:

5' TAATACGACTCACTATA 3'
3' ATTATGCTGAGTGATAT 5' (Seq. ID Nos. 3 and 4)

The sequence of the SP6 RNA polymerase promoter (described in the prior art) is:

5' ATTTAGGTGACACTATA 3'

3' TAAATCCACTGTGATAT 5' (Seq. ID Nos. 5 and 6)

It is desirable that at least one of the probes in the complex comprises a "template portion" which may be used as a template by a polymerase which recognises the promoter formed in the complex, such that the formation of the complex of the invention can allow for the synthesis of newly-synthesised ribonucleic acid, which can be detected directly or indirectly in any of a number of ways which will be apparent to those skilled in the art. The template portion is advantageously present on the promoter strand.

It will generally be preferred for the 3' end of the promoter strand to be blocked in some way, so that RNA polymerase-mediated extension thereof is not possible. This is especially desirable where the promoter strand comprises a target complementary portion. Blocking of the 3' end is conveniently accomplished by providing a phosphate group, or a propyl group, instead of an -OH group, on the 3' terminal nucleotide. Other methods of blocking the 3' end are well known to those skilled in the art.

The present inventors have found that the efficiency of initiation of RNA synthesis by the RNA polymerase promoter is affected by sequences adjacent to the promoter, downstream. In particular, a region of twelve bases (the "+12 region") is required for optimum RNA transcription. It is therefore preferred that the template portion of the complex, which is transcribed, comprises a +12 region appropriate to the polymerase which recognises the promoter. The inventors have elucidated the optimum sequence of +12 regions for the T7 polymerase (discussed in greater detail below) - it is not known at present if these are also optimum for, say, T3 and SP6 polymerases. If, as is possible, SP6 and T3 polymerases have different optimum +12 regions, it would be a simple matter for the person skilled in the art to identify the relevant sequence by trial-and-error, with the benefit of the present disclosure.

The sequences of preferred +12 regions, for inclusion in the template portion of the

promoter strand, (in respect of T7 polymerase) are shown below in Table 1. The most active +12 region (giving greatest transcription) is at the top, with the other sequences shown in decreasing order of preference.

Table 1 Alternative template +1 to +12 sequences for T7 polymerase, in descending order of transcription efficiency (Seq. ID Nos. 7-15 respectively).

5' GTTCTCTCTCCC 3'
5' GCTCTCTCTCCC 3'
5' GTTGTGTCTCCC 3'
5' GATGTGTCTCCC 3'
5' ATCCTCTCTCCC 3'
5' GTTCTCGTGCCC 3'
5' ATCCTCGTGCCC 3'
5' GCTCTCGTGCCC 3'
5' GTTGTGGTGCCC 3'

(The 5' base is numbered as +1, being the first base downstream from the end of the promoter sequence, the 3' base as +12).

In a further embodiment, the template portion of the complex (preferably on the promoter strand) could contain sequences that can be used to identify, detect or amplify the *de novo* synthesised RNA copies (see, for example, WO 93/06240, US 5,554,516, or, for example, using molecular beacon sequences such as those disclosed by Tyagi & Kramer 1996 Nature Biotech 14, 303-308). These sequences are conveniently placed adjacent to, and downstream of, a +12 region (as described above) and may comprise, but are not limited to, one or more of the following: unique "molecular beacon" sequences; capture sequences; detection probe complementary sequences; alternative RNA promoter sequences for use in an isothermal amplification cycling reaction (see below). A particular unique sequence especially useful in the present invention is provided by bases 791-820 of 16S ribosomal RNA from *Streptomyces brasiliensis* (Stackebrandt *et al*, 1991 Appl. Environ. Microbiol. 57, 1468-1477), which sequence has no alignment with any known human DNA or DNA of a known human pathogen.

In a further embodiment of the invention it may be advantageous, when seeking to detect a sequence of interest in a mixture comprising double stranded DNA (such as genomic DNA), to include in the hybridisation mixture one or more of further oligonucleotides ("blocking oligonucleotides"). These blocking oligonucleotides (preferably provided as a pair) hybridise to the sequence of interest, typically on each side of the portion which is complementary to the first probe (and the portion complementary to the second probe, if the second probe comprises a target-complementary portion). The blocking oligonucleotides preferably comprise DNA, PNA, LNA (or a combination thereof) and advantageously each comprise at least 10 (more preferably at least 20) nucleotides. The purpose of the blocking oligonucleotides is to inhibit (under the hybridisation conditions employed) re-annealing of the target strand with its complementary strand. The blocking oligonucleotides may anneal to the target strand substantially adjacent to the first and second probes, or may anneal at a distance (e.g. 5-50 bases) therefrom.

Blocking oligonucleotides may offer little advantage if the first and/or second probes contain large target-complementary "feet" regions.

Detection Methods

RNA produced in accordance with the method of the invention could be detected in a number of ways, preferably following amplification (most preferably by means of an isothermal amplification step). For example, newly-synthesised RNA could be detected in a conventional manner (e.g. by gel electrophoresis), with or without incorporation of labelled bases during the synthesis.

Alternatively, for example, newly-synthesised RNA could be captured at a solid surface (e.g. on a bead, or in a microtitre plate), and the captured molecule detected by hybridisation with a labelled nucleic acid probe (e.g. radio-labelled, or more preferably labelled with an enzyme, chromophore, fluorophore and the like).

One preferred detection method involves the use of molecular beacons or the techniques of fluorescence resonance energy transfer ("FRET"), delayed fluorescence energy transfer

("DEFRET") or homogeneous time-resolved fluorescence ("HTRF"). Molecular beacons are molecules which a fluorescence signal may or may not be generated, depending on the conformation of the molecule. Typically, one part of the molecule will comprise a fluorophore, and another part of the molecule will comprise a "quencher" to quench fluorescence from the fluorophore. Thus, when the conformation of the molecule is such that the fluorophore and quencher are in close proximity, the molecular beacon does not fluoresce, but when the fluorophore and the quencher are relatively widely-separated, the molecule does fluoresce. The molecular beacon conveniently comprises a nucleic acid molecule labelled with an appropriate fluorophore and quencher.

One manner in which the conformation of the molecular beacon can be altered is by hybridisation to a nucleic acid, for example inducing looping out of parts of the molecular beacon. Alternatively, the molecular beacon may initially be in a hair-pin type structure (stabilised by self-complementary base-pairing), which structure is altered by hybridisation, or by cleavage by an enzyme or ribozyme.

FRET (Fluorescence Resonance Energy Transfer) occurs when a fluorescent donor molecule transfers energy via a nonradiative dipole-dipole interaction to an acceptor molecule. Upon energy transfer, which depends on the R^{-6} distance between the donor and acceptor, the donor's lifetime and quantum yield are reduced and the acceptor fluorescence is increased or sensitised.

The inventors have used FAM (6-carboxyfluorescein) and TAMRA (N,N,N',N'-tetramethyl-6-carboxy rhodamine) as donor and acceptor in a nucleic acid hybridisation assay. The assay uses two dye labelled DNA oligomers (15 mers). FAM is linked to the 5' of one probe and TAMRA to the 3' of the other. When hybridised to target nucleic acid the probes are positioned adjacent to one another and FRET can occur. The inventors' experiments have demonstrated that for maximum signal the probes need to be spaced by five bases.

Another approach (DEFRET, Delayed Fluorescence Energy Transfer) has been to exploit the unique properties of certain metal ions (Lanthanides e.g. Europium) that can exhibit

efficient long lived emission when raised to their excited states ($\lambda_{\text{excitation}} = 337 \text{ nm}$, $\lambda_{\text{emission}} = 620 \text{ nm}$). The advantage of such long lived emission is the ability to use time resolved (TR) techniques in which measurement of the emission is started after an initial pause, so allowing all the background fluorescence and light scattering to dissipate. Cy5 (Amersham Pharmacia) ($\lambda_{\text{excitation}} = 620 \text{ nm}$, $\lambda_{\text{emission}} = 665 \text{ nm}$) can be used as the DEFRET partner.

HTRF (see WO92/01224; US 5,534,622) occurs where the donor (Europium) is encapsulated in a protective cage (cryptate) and attached to the 5' end of an oligomer. The acceptor molecule that has been developed for this system is a protein fluorophore, called XL665. This molecule is linked to the 3' end of a second probe. This system has been developed by Packard.

In another embodiment, the newly-synthesised RNA, before or after amplification, results in formation of a ribozyme, which can be detected by cleavage of a particular nucleic acid substrate sequence (e.g. cleavage of a fluorophore/quencher dual-labelled oligonucleotide).

Amplification techniques

In preferred embodiments of the present invention, the RNA derived from the target dependent transcription reaction is amplified prior to detection, the amplification step typically requiring the introduction of a DNA oligonucleotide. The amplification step is advantageously effected isothermally (i.e. without requiring thermal cycling of the sort essential in performing PCR). The introduced DNA oligonucleotide is complementary to the 3' region of the newly synthesised RNA and also contains the sequence of an RNA polymerase promoter and a unique transcribable sequence (template portion). Upon hybridisation of the newly-synthesised RNA with the DNA oligonucleotide, a primer extension reaction from the 3' end of the RNA, mediated by an added DNA polymerase, produces a functional double stranded RNA polymerase promoter. In the presence of the relevant RNA polymerase, multiple copies of a second RNA species are synthesised from the unique region of the DNA oligonucleotide. This RNA in turn can act as primer to a further round of primer extension and RNA synthesis. The synthesis of further RNA

requires the presence of another DNA oligonucleotide that is complementary to the 3' region of the second RNA species. This DNA oligonucleotide also contains the sequence of an RNA polymerase promoter element together with a sequence upon transcription of which produces RNA comprising sequences identical to that derived in the target dependent transcription reaction. The 3' end of the RNA thus synthesised is complementary to the first DNA oligonucleotide and hence a cyclical amplification system is generated (see Figure 3).

In these embodiments, it is important that the RNA promoter(s) formed during the amplification step(s) is (are) selected to be recognised by a polymerase different to that which recognises the split promoter formed initially at the 2½ or 3 way junction, so as to avoid inadvertent formation of a complete promoter *ab initio*, which would give a very high background signal.

In a variant of the embodiment described above, the introduced DNA oligonucleotide hybridises to the *de novo* synthesised RNA, the respective sequences being such that a further RNA polymerase promoter is directly formed without the need for a DNA polymerase-mediated extension step (see Figure 13). A cycling reaction may then be performed essentially as described above, with the transcript from one reaction hybridising with a DNA oligonucleotide to form a second RNA promoter, which produces a transcript comprising a sequence common to the original transcript.

In a further variant, an RNA species produced from a split promoter in turn comprises the first few bases of an RNA polymerase promoter, such that the RNA may in turn be the target sequence for the formation of a second split promoter (at a 2½ or 3 way junction), leading to synthesis of a further RNA species. If desired the sequences of the template portions can be selected so as to create an amplification cycle in which the RNA transcript from one split promoter forms the target for the creation of a second split promoter, which produces a transcript which re-forms the first split promoter. The scheme is illustrated schematically in Figure 15. It will be appreciated that, in an amplification cycle of this sort, there is no requirement to use a different RNA promoter sequence to that in the original 2½ or 3 way junction, because the method would not create a fully double-

stranded RNA promoter *ab initio*, in the absence of target.

The above system could be arranged such that an RNA transcript comprised a plurality of portions of RNA promoters, so as to be capable of forming a plurality of split promoters in a single cycle, thereby increasing the amount of amplification. Similarly, in the other types of amplification cycles described above, the added oligonucleotides could, if desired, be capable of forming a plurality of RNA promoters.

In the above amplification strategies, some background "noise" may be created because of the tendency of many RNA polymerases (at relatively low frequency) to produce RNA transcripts of a single stranded DNA sequence such that, for example, referring to Figure 3, some transcription of DNA oligonucleotides (16) and (22) may occur even in the respective absence of RNA molecules (14) and (20); or, the same phenomenon may occur, with reference to Figure 13, in the absence of RNA molecules (14) and (52). It is possible that this low level of background transcription can be reduced by designing the DNA oligonucleotides (16 and 22 in Figure 3; 50 and 54 in Figure 13) so as to incorporate near their 3' end a sequence which tends to cause termination of transcription. One example of such a sequence, which is especially effective at terminating T7 polymerase-mediated transcription, is AACAGAT (in the template strand), as disclosed by He *et al.*, (1998 J. Biol. Chem. **273**, 18,802). The same or a similar termination sequence could be positioned at the 5' end of the DNA template to increase processivity.

Various embodiments of the invention will now be described by way of illustrative examples and with reference to the accompanying drawings, in which:

Figure 1 is a schematic representations of a complex in accordance with the invention, comprising a "three way" junction;

Figures 2, 4, 6-9, 11 and 12 are schematic representations of a complex in accordance with the invention, comprising a " $2\frac{1}{2}$ way" junction;

Figures 3, 13 and 15 are schematic representations of a method of detecting a target

sequence of interest by amplifying nucleic acid synthesis;

Figure 5 is a bar chart showing relative fluorescence units present following various nucleic acid amplification reactions; and

Figures 10 and 14 are bar charts showing picomoles of RNA produced following various nucleic acid amplification reactions.

Figure 1 shows a complex in accordance with the invention. The complex comprises a promoter complementary strand "CS" (2), a promoter strand "PS" (4), and a target strand (6). The CS (2) comprises the full length sequence of a first strand of a double stranded promoter (marked "Pr" in the figure). The target strand (6) comprises three bases which are an end part (8) of a second strand of the double stranded promoter which is complementary to part of the CS (2). The PS (4) comprises the rest of the second strand of the double stranded promoter, which part is complementary to the first strand of the promoter provided on the CS (2). Hybridisation of the CS (2) to the target strand (6), or hybridisation of the CS (2) to the PS (4), is not sufficient to constitute a functional, double stranded promoter. However, a substantially functional promoter is formed upon hybridisation of the CS (2) with both the target strand (6) and the PS (4), which represents a complex in accordance with the present invention.

In the embodiment shown in Figure 1, the PS (4) comprises a portion (10) which is complementary to the target strand (6), such that the complex forms what may be described as a "three way junction". In an alternative embodiment, illustrated schematically in Figure 2, the PS (4) does not comprise a portion complementary to the target strand (6), such that the complex forms what may be described as a "two-and-a-half way junction" ($2\frac{1}{2}$ way junction).

In both of the embodiments illustrated in Figures 1 and 2, the PS (4) comprises a template portion (12), which can act as a template nucleic acid strand for *de novo* nucleic acid synthesis once the functional promoter has been formed. Template portion (12) also preferably comprises a +12 region to optimise efficiency of transcription by the RNA

polymerase. The newly-synthesised nucleic acid is conveniently RNA, synthesised under the influence of an RNA polymerase promoter, such that multiple RNA transcripts (14) of the template portion (12) are formed.

The *de novo* synthesised nucleic acid (14) may be detected directly or indirectly. Preferably the *de novo* synthesised nucleic acid (14) is subjected to an amplification process prior to detection. A large number of suitable detection methods will be apparent to those skilled in the art. For example, the *de novo* synthesised nucleic acid (14) might hybridise to a complementary oligonucleotide molecular beacon sequence (e.g. as described by Tyagi & Kramer, 1996 Nature Biotechnology 14, 303-308), such that *de novo* nucleic acid synthesis leads to an increase, or a decrease as appropriate, in a fluorescence signal. Alternatively, the template portion (12) may be appropriately selected such that DNA or RNA molecules synthesised with the portion (12) as a template may comprise, for example, capture sequences or detection sequences.

As mentioned above, the *de novo* synthesised nucleic acid is preferably subjected to an amplification step prior to detection. The amplification step is such that a small amount of *de novo* synthesised nucleic acid results in the generation of a large amount of signal. Desirably, the amplification step is accomplished by performing two or more nucleic acid synthesis steps in a cyclical manner, such that the nucleic acid product of a first synthesis step acts as the primer for a second nucleic acid synthesis step, the product of which acts as the primer for the first nucleic acid synthesis step, and so on. Cycling amplification of this sort is disclosed in WO93/06240.

Figure 3 is a schematic representation of an embodiment of a cyclical nucleic acid synthesis, resulting in nucleic acid amplification. In Figure 3, the 3' end of a *de novo* synthesised RNA transcript (14) produced from the template portion (12) of the second probe (4), is hybridised to an added DNA oligonucleotide (16). In step (i) the 3' end of the transcript (14) is extended by the addition of ribonucleotides and/or deoxyribonucleotides in the presence of an appropriate polymerase. In the illustrated embodiment the extended portion (of the transcript (14)) is of course complementary to the oligonucleotide (16) and forms an active double stranded RNA promoter (18) which

is recognised by the appropriate RNA polymerase, so as to produce multiple copies of a second RNA species (20) which is a transcript of the 5' end of the DNA oligonucleotide (16).

In turn, the 3' end of the RNA molecules (20) can hybridise to a further added DNA oligonucleotide (22) (step (ii)). As previously, the 3' end of the RNA molecule (20) can undergo primer extension (step iii) by the addition of ribo- or (preferably) deoxyribonucleotides, thereby forming an active double stranded RNA promoter (24), which is recognised by the relevant RNA polymerase which produces multiple copies of an RNA molecule which is a transcript of the 5' end of the DNA oligonucleotide (22).

The sequence of the DNA oligonucleotides (16) and (22) is preferably selected such that the RNA transcripts produced from the oligonucleotide (22) comprise sequences which are identical to those present in the RNA transcripts (14) produced originally, such that a cycle is formed (step iv), in which the most recently synthesised RNA molecules can hybridise to DNA oligonucleotide (16), be extended to form the RNA promoter (18) and so on. In this way, massive amplification of the original transcript (14) may be achieved, thereby greatly enhancing the sensitivity of the detection method of the invention.

Figure 15 is a schematic representation of an amplification cycle in which a *de novo* synthesised RNA transcript (14), from a split promoter formed by the presence of the sequence of interest, hybridises to first and second probes (60, 62 respectively) to form a second split promoter (indicated generally at 64). The sequence of the template portion of second probe (62) is such that the RNA transcript (66) from split promoter (64), can act as target for a further pair of first and second probes (68, 70 respectively) creating a third split promoter (indicated generally at 72). The sequence of the template portion of the second probe (70) is such that the RNA transcript produced by split promoter (72) has substantially the same sequence as the original RNA molecule (14), so that the second split promoter (64) can be reformed, thereby creating an amplification cycle.

Examples

Example 1: Transcription from a split T7 RNA Polymerase promoter at a 2½ way junction.

This example demonstrates the creation of a functional DNA dependent RNA polymerase promoter as a result of the formation of a 2½ way junction comprising target nucleic acid (Target: wild type human DNA cystic fibrosis transmembrane conductance regulator gene (CFTR) in which a deletion of TTT causes a cystic fibrosis-encoding mutation $\Delta F508$), a partly complementary oligonucleotide (complementary strand) and a promoter strand. In the example, the target sequence is provided by a synthetic oligonucleotide, which serves to demonstrate the principle of the invention. In practice, the target sequence would comprise a complex mixture of chromosomal DNA.

The example is illustrated schematically in Figure 4. The complete T7 promoter is located towards the 3' end of promoter complementary strand probe (2). The first three (5') bases of the promoter sequence are complemented by three bases (3'ATT 5') (8), in target strand (6), and probe (2) hybridises to the target (6) in such a way that the 3'TTT5' in the wild type is 14 bases downstream from the start of the promoter. Hybridisation of a promoter strand probe (4), (at the 3' end of which is the complement to the T7 promoter minus three bases) to probe (2) forms a double stranded promoter, made complete by the three bases (8) in target (6), and therefore a split promoter is formed to yield a *de novo* synthesised RNA (14) in the presence of T7 RNA polymerase. For convenience, the promoter strand probe (4) is referred to hereafter as the PS probe, and the promoter complementary strand probe (2) is referred to hereafter as the CS probe.

1.1 Preparation of Oligonucleotides

The target oligonucleotides and probes were synthesised by phosphoramidite chemistry using an Applied Biosystems 380A synthesiser, used according to the manufacturer's instructions. All oligonucleotides were HPLC purified using standard techniques.

1.2 Split promoter probe and RNA synthesis

Hybridisation reactions comprised mixtures of DNA including target oligonucleotide (6), PS and CS probes, together with relevant controls comprising mixtures with and without target/probes. For hybridisation reactions, 40 fmol of target oligonucleotide was mixed

with 40 fmol of PS probe and 40 fmol of CS probe in a solution containing 4 μ l 5x T7 RNA polymerase buffer (from Promega, giving 1x concentrations of 40mM Tris (pH7.9), 6 mM $MgCl_2$, 2 mM spermidine and 10 mM NaCl) and distilled water to a final volume of 20 μ l (following final addition of T7 RNA polymerase and rNTP mix). In this example, and others in the present specification, Milligan's buffer (Milligan *et al.* 1987 Nucl. Acids Res. 15, 8783-8798) may be used in place of Promega RNA polymerase buffer. Indeed, in those examples where no DNA polymerase (e.g. where there is no DNA polymerase-dependent primer extension amplification step) is used, Milligan's buffer may be preferred. The composition of Milligan's buffer is as follows: 20mM $MgCl_2$, 5mM DTT, 80mg/ml PEG, 50 μ g/ml BSA, 0.01% (v/v) Triton X-100, 1mM spermidine, and 40mM Tris HCl, pH8.1.

The mixture was heated to 90°C for 3 minutes to denature the nucleic acids, incubated on ice for 2 minutes, and equilibrated to 37°C for 1 minute. Probes were annealed and transcribed at 37°C for 180 minutes by addition of 40 units of T7 RNA polymerase (Promega) and 40 nmoles rNTP mix (Pharmacia Biotech). DNA oligonucleotides were removed from the reaction mix by the addition of 4 units of DNase I (Ambion) and incubating at 37°C for 20 minutes prior to end detection. The resulting product was immobilised by hybridisation to a specific biotinylated oligonucleotide (probe 3) which was in turn bound to a streptavidin coated well. The immobilised product was detected by time resolved fluorescence via the hybridisation of probe 4, a europium labelled oligonucleotide probe (see below).

1.3 Detection of RNA by Time Resolved Fluorescence (TRF)

5 μ l of reaction sample was added to the reaction mix consisting of 145 μ l of Wallac (E.G. & G. Wallac, Crown Hill Business Centre, Milton Keynes, UK) assay buffer, 0.9 pmol of probe 3 and 0.3 pmol of probe 4 in a well of a Labsystems streptavidin coated microtitre plate, which was incubated at room temperature for 60 minutes (N.B. the use of longer probe PS gives a transcript with a longer capture tail, so that capture of this with the extended biotinylated probe 3a results in more sensitive detection). Unbound material was removed by washing the wells 4x with 200 μ l of Wallac wash solution. 180 μ l of Wallac enhancement solution was added to dissociate the europium from its chelated

bonding to probe 4, and TRF was measured every 10 minutes up to 60 minutes using the europium protocol on a Wallac Victor 1420 Multilabel Counter. The results obtained (using Probes PSa and 3a) are shown in Figure 5.

1.4 List of oligonucleotides

In general, in the oligonucleotide sequences disclosed in Example 1 and the successive examples below: lower case letters denote the site of the $\Delta F508$ mutation; promoter portions are shown underlined; portions of probes used for detection purposes are indicated by italics; and capture portions are shown in bold face. The 3' phosphate groups on PS probes (where included) are optional.

Target oligonucleotide (Normal wild type CFTR DNA)

5' TTATGCCTGGCACCATTAAAGAAAATATCATCmGGTGTTTCCTATGATGA
ATATAGATACAGAAGCGTCATCAAAGC 3' (Seq. ID No. 16)

CS probe (T7 promoter)

5' ATAGGAAACACCAAAGATGATATTTTCTTTAATACGACTCACTATA 3'
(Seq. ID No. 17)

PS probe (T7 promoter with 3' ATT 5' start sequence in target, and template portion)

5' CCTTGTCTCCGTTCTGGATATCACCCGATGTGTCTCCCTATAGTGAGTCGT
A 3' (Seq. ID No. 18)

PSa probe (T7 promoter with 3' ATT 5' start sequence in target, and template portion with capture tail extended to 20 bases for more sensitive capture and detection, using probe 3a)

5' TGCCTCCTTGTCTCCGTTCTGGATATCACCCGATGTGTCTCCCTATAGTGAG
TCGTA phosphate 3' (Seq. ID No. 19)

Probe 3 (with 5' biotin to allow capture on streptavidin coated plates)

5' TGCCTCCTTGTCTCCGTTCT 3' (Seq. ID No. 20)

Probe 3a (version of probe 3a extended by 5 bases to allow more sensitive capture of

transcript from probe PSa)

5' TCCGCTGCCTCCTTGTCTCCGTTCT 3' (Seq. ID No. 21)

Probe 4 (europium-labelled)

5' GGATATCACCCG 3' (Seq. ID No. 22)

Example 2: Transcription from a split T3 RNA Polymerase promoter at a 2½ way junction at ΔF508

The example is illustrated schematically in Figure 6. The complete T3 promoter is located towards the 3' end of the CS probe (2). The first three bases of the T3 RNA polymerase promoter (5'AAA3') in the CS probe (2) anneals to the 3'TTT5' ΔF508 site (8) in the wild type target (6), and therefore the ΔF508 mutation will result in loss of the split promoter start, with subsequent loss of transcription. Hybridisation of a PS probe (4), (at the 3' end of which is the complement to the T3 promoter minus three bases) to CS probe (2) forms a double stranded promoter, made complete by the three bases (3' TTT 5') in the target, and therefore a split promoter is formed to yield a *de novo* synthesised RNA (14) in the presence of T3 RNA polymerase.

2.1 Preparation of Oligonucleotides

The target oligonucleotides and probes are synthesised and purified as described in Example 1.

2.2 Split promoter probe and RNA synthesis

Hybridisation reactions comprise mixtures of DNA including target oligonucleotide, PS and CS probes, together with relevant controls comprising mixtures with and without target/probes PS and CS. Hybridisation reactions are established as described in Example 1.2, but using the probe sequences detailed below and T3 RNA polymerase/buffer (Promega). The hybridisation mixture is then treated as described in Example 1, but using probe 3 and probe 4 sequences detailed below.

2.3 Detection of RNA by Time Resolved Fluorescence (TRF)

5μl of reaction sample is added to the reaction mix consisting of 145 μl of Wallac assay

buffer, 0.9 pmol of probe 3 and 0.3 pmol of probe 4 in a well of a Labsystems streptavidin coated microtitre plate, which is incubated at room temperature for 60 minutes. The assay is then performed as described above (at Example 1.3).

2.4 List of oligonucleotides

Target oligonucleotide (Normal wild type DNA)

5' TTATGCCTGGCACCATTAAAGAAAATATCATCtttGGTGTTCCTATGATGA
ATATAGATACAGAAGCGTCATCAAAGC 3' (Seq. ID No. 16)

CS Probe (T3 promoter) (Seq. ID No. 23)

5' CTGTATCTATATTCATCATAGGAAACACCAAATTAACCCTCACTAAA 3'

PS Probe (T3 promoter with 3' TTT 5' start sequence in target, and template portion)

5' CCTTGTCTCCGTTCTGGATATCACCCGATGTGATTCCCTTTAGTGAGGGTTA
A phosphate 3' (Seq. ID No. 24)

Probe 3 (with 5' biotin to allow capture on streptavidin coated plates)

5' TGCCTCCTTGTCTCCGTTCT 3' (Seq. ID No. 20)

Probe 4 (europium-labelled)

5' GGATATCACCCG 3' (Seq. ID. No. 22)

Example 3: Transcription from a split T3 RNA Polymerase promoter at a 2½ way junction

The example is illustrated schematically in Figure 7. The complete T3 promoter (the first three bases of which is 5' TTA 3', a different version to that in example 2) is located towards the 3' end of the CS probe (2). The first three (5') bases of the promoter sequence is complemented by three bases (3' AAT 5'), (8) in the target (6) (Target: Hepatitis B (Hep B) DNA). Hybridisation of a PS probe (4), (at the 3' end of which is the complement to the T3 promoter minus three bases) to CS probe (2) forms a double stranded promoter, made complete by the three bases (3' AAT 5') in the target (6), and therefore a split promoter is formed to yield a *de novo* synthesised RNA in the presence

The target oligonucleotides and probes were synthesised and purified as described in Example 1.

Hybridisation reactions are established as described in Example 2.2 and treated as described in Example 1.2 above, but using the nucleic acid sequences detailed below. The resulting product is detected by the hybridisation of molecular beacon (see below).

5 μ l of reaction sample is added to the reaction mix consisting of 145 μ l of hybridisation solution and 2 pmol molecular beacon (fluorophore = FAM; quencher = methyl red), in a Labsystems White Microstrip microtitre plate, which is incubated in the dark at room temperature for 60 minutes. Fluorescence signal from the hybridised beacon/target is measured using the Wallac Victor 1420 Multilabel Counter, using the fluorescein protocol.

5' GAGGCATAGCAGCAGGATGAAGAGGAAGATGATAAAACGCCGCAGACACA
TCCAGCGATAACCAGGACAGGTTGGAGGACAGGA 3' (Seq. ID No. 25)

5' TGGTTATCGCTGGATGTGTCTGCGGCGTTTTATTAACCCTCACTAAA 3'
(Seq. ID No. 26)

5' GTTCTATCCTGCACCGCCGGAGCTTTCACCCCTTCCCTTTAGTGAGGGTTA A phosphate 3' (Seq. ID No. 27)

Molecular Beacon Oligonucleotide probe (comprising a sequence derived from *Streptomyces thermoalkatolerans*, with complementary 5' and 3' ends)

5' CGCGATCCTGCACCGCCGGAGCTTTCCACCCGCG 3' (Seq. ID No. 28)

Example 4: Transcription from a split SP6 promoter at a 2½ way junction

In this example, the target is wild type human DNA CFTR gene in which a deletion of TTT causes a cystic fibrosis-encoding mutation $\Delta F508$.

The example is illustrated schematically in Figure 8. The complete SP6 promoter is located towards the 3' end of the CS probe (2). The first three (5') bases of the promoter sequence is complemented by three bases (3' TAA 5') (8) in the target (6), and the CS probe (2) hybridises to the target (6) in such a way that the 3' TTT 5' in the wild type is 6 bases downstream from the start of the promoter. Hybridisation of a PS probe (4), (at the 3' end of which is the complement to the SP6 promoter minus three bases) to CS probe (2) forms a double stranded promoter, made complete by the three bases (3'TAA 5') in the target, and therefore a split promoter is formed to yield a *de novo* synthesised RNA (14) in the presence of SP6 RNA polymerase.

4.1 Preparation of Oligonucleotides

The target oligonucleotides and probes are synthesised and purified as described in Example 1.

4.2 Split promoter probe and RNA synthesis

Hybridisation reactions are established and treated as described in Example 1.2, but using the nucleic acid sequences detailed below and using SP6 RNA polymerase/buffer (Promega).

4.3 Detection of RNA by Time Resolved Fluorescence (TRF)

5 μ l of reaction sample is added to the reaction mix consisting of 145 μ l of Wallac assay buffer, 0.9 pmol of probe 3 and 0.3 pmol of probe 4 in a well of a Labsystems streptavidin coated microtitre plate, which is incubated at room temperature for 60 minutes. The assay is then performed as described above (at section 1.3).

4.4 List of oligonucleotides

Target oligonucleotide (Normal wild type DNA)

5' TTATGCCTGGCACCATTAAAGAAAATATCATCtttGGTGTTCCTATGATGA
ATATAGATACAGAAGCGTCATCAAAGC 3' (Seq. ID No. 16)

CS Probe (SP6 promoter)

5' ATTCATCATAGGAAACACCAAAGATGATATTTAGGTGACACTATA 3' (Seq. ID No. 29)

PS Probe (SP6 promoter with 3'TAA5' start sequence in target, and template portion)

5' CCTTGTCTCCGTTCTGGATATCACCCGATGTGGTATTCTTATAGTGTCACCT
A phosphate 3' (Seq. ID No. 30)

Probe 3 (with 5' biotin to allow capture on streptavidin coated plates)

5' TGCCTCCTTGTCTCCGTTCT 3' (Seq. ID No. 20)

Probe 4 (europium-labelled)

5' GGATATCACCCG 3' (Seq. ID No. 31)

Example 5: Transcription from a split SP6 RNA Polymerase promoter at a 2½ way junction at ΔF508

The example is illustrated schematically in Figures 9A and 9B. One conformation of the ΔF508 CFTR mutation results in the loss of a 3' GAA 5' from the sequence 3' TAGAAA 5', resulting in the creation of a 3' TAA 5' triplet (8) and thus an SP6 promoter start sequence (Figure 9B). Hence a functional SP6 promoter is created using CS probe (2) and PS probe (4) with CFTR mutant DNA target (6), whereas no functional promoter is created using PS and CS probes with normal wild type DNA target (Figure 9A). Hybridisation of a PS probe (4), (at the 3' end of which is the complement to the SP6 promoter minus three bases) to CS probe (2) forms a double stranded promoter, made complete by the three bases (3' TAA 5') in the mutant target (6), and therefore a split promoter is formed to yield a *de novo* synthesised RNA in the presence of SP6 RNA polymerase.

5.1 Preparation of Oligonucleotides

The target oligonucleotides and probes are synthesised and purified as described in Example 1.

5.2 Split promoter probe and RNA synthesis

Hybridisation reactions are established and treated as described in Example 1.2, but using the nucleic acid sequences detailed below and using SP6 RNA polymerase/buffer (Promega).

5.3 Detection of RNA by Time Resolved Fluorescence (TRF)

5 µl of reaction sample is added to the reaction mix consisting of 145 µl of Wallac assay buffer, 0.9 pmol of probe 3 and 0.3 pmol of probe 4 in a well of a Labsystems streptavidin coated microtitre plate, which is incubated at room temperature for 60 minutes. The assay is then performed as described above (section 1.3).

5.4 List of oligonucleotides

Target oligonucleotide (Normal wild type DNA, no $\Delta F508$ deletion)

5' GTTGGCATGCTTTGATGACGCTTCTGTATCTATATTCATCATAGGAAACACC
AaagATGATATTTTCTTTAATGGTGCCAGGCATAATCCAGGAAAACCTGAGAAC
AGAATGAAATTCTTC 3' (Seq. ID No. 32)

Target oligonucleotide (CF mutant DNA, with the $\Delta F508$ deletion)

5' GTTGGCATGCTTTGATGACGCTTCTGTATCTATATTCATCATAGGAAACACC_a
atGATATTTTCTTTAATGGTGCCAGGCATAATCCAGGAAAACCTGAGAACAGAA
TGAAATTCTTC 3' (Seq. ID No. 33)

CS Probe (SP6 promoter)

5' TTATGCCTGGCACCATTAAAGAAAATATCATTTAGGTGACACTATA 3'
(Seq. ID No. 34)

PS Probe (SP6 promoter with 3' TAA 5' start sequence formed by a $\Delta F508$ mutation in CFTR mutant DNA, and template portion)

5' CCTTGTCTCCGTTCTGGATATCACCCGATGTGGTATTCTATAGTGTCACCT

A phosphate 3' (Seq. ID No. 30)

Probe 3 (with 5' biotin to allow capture on streptavidin coated plates)

5' TGCCTCCTTGTCTCCGTTCT 3' (Seq. ID No. 20)

Probe 4 (europium-labelled)

5' GGATATCACCCG 3' (Seq. ID No. 22)

Example 6: Transcription from a split T7 RNA Polymerase promoter at a 3 way junction

In this example, the target is wild type human DNA CFTR gene, at which a deletion of TTT causes a cystic fibrosis-encoding mutation $\Delta F508$.

The complete T7 promoter is located towards the 3' end of a CS probe. The first three (5') bases of this sequence complement three bases in the target. Hybridisation of a PS probe, (which has the complement to the T7 promoter minus three bases, and a complement to the target DNA) to CS probe and the target forms a double stranded promoter, made complete by the three bases in the target, and therefore a split promoter is formed to yield a *de novo* synthesised RNA in the presence of T7 RNA polymerase.

6.1 Preparation of Oligonucleotides

The target oligonucleotide and probes were synthesised and purified as described in Example 1.

6.2 Split promoter probe and RNA synthesis

Hybridisation reactions were established and treated as described in Example 1.2, but using the nucleic acid sequences detailed below. The resulting product was immobilised by hybridisation to a specific biotinylated oligonucleotide (probe 3) which was in turn bound to a streptavidin coated well of a microtitre plate. The immobilised product was detected by colorimetry via the hybridisation of probe 4, an alkaline phosphatase-labelled oligonucleotide probe (see below).

6.3 Detection of RNA by Colorimetry

5 μ l of reaction sample was added to the reaction mix consisting of 145 μ l hybridisation buffer (20 mM EDTA pH 8.0, 1 M NaCl, 50 mM Tris, 0.1% bovine serum albumin, mixture adjusted to pH 8.0 with HCl), 0.9 pmol of probe 3 and 12.7 pmol of probe 4 in a well of a Labsystems streptavidin coated microtitre plate, which was incubated at room temperature for 60 minutes. Unbound material was removed by washing the wells 4x with 200 μ l of wash solution (0.25 M Tris, 0.69 M NaCl, 13.4 mM KCl, adjusted to pH 8.0 with HCl), and 1x with substrate buffer (used as a 1x solution, made from a 5x concentrate stock obtained from Boehringer Mannheim 726915). 180 μ l of substrate buffer containing 5 mg/ml of 4-nitrophenyl phosphate was added the well, and colour development was measured by optical density at 405 nm using a Labsystems integrated EIA Management system plate reader, readings taken every 2 minutes for 30 minutes. The results obtained are shown in Figure 10.

6.4 List of oligonucleotides

Target oligonucleotide (Normal wild type DNA)

5' GTTGGCATGCTTTGATGACGCTTCTGTATCTATATTCATCATAGGAAACACC
aaaGATGATATTTTCTTTAATGGTGCCAGGCATAATCCAGGAAAACACTGAGAA
CAGAATGAAATTCTTC 3' (Seq. ID No. 32)

CS Probe (T7 promoter)

5' CAGTTTTCTGGATTATGCCTGGCACCATTAAATACGACTCACTATA 3'
(Seq. ID No. 35)

PS Probe (T7 promoter with 3' ATT 5' start sequence in target, and template portion)

5' CCTTGTCTCCGTTCTGGATATCACCCGATGTGTCTCCCTATAGTGAGTCGTA
AGAAAATATCATCTTTGGTGTTCCTATGATG 3' (Seq. ID No. 36)

Probe 3 (with 5' biotin to allow capture on streptavidin coated plates)

5' TGCCTCCTTGTCTCCGTTCT 3' (Seq. ID No. 20)

Probe 4 (alkaline phosphatase-labelled)

5' GGATATCACCCGATGTG 3' (Seq. ID No. 37)

Example 7: Transcription from a split T7 RNA Polymerase promoter, and amplification without the use of DNA polymerase extension

This example demonstrates the creation of a functional DNA dependent RNA polymerase promoter as a result of the formation of a nucleic acid complex comprising target nucleic acid (Target: wild type human DNA: cystic fibrosis transmembrane conductance regulator gene (CFTR) at which a deletion of TTT causes a cystic fibrosis-encoding mutation $\Delta F508$), a partly complementary oligonucleotide and a promoter strand probe.

The example is illustrated schematically in Figure 12. The complete T7 promoter is located towards the 3' end of a CS probe (2). The first three (5') bases of the promoter sequence is complemented by three bases (3' ATT 5') (8) in target (6), and CS probe (2) hybridises to target (6) in such a way that the 3' TTT 5' in the wild type sequence is 14 bases downstream from the start of the promoter. Hybridisation of a PS probe (4), (at the 3' end of which is the complement to the T7 promoter minus three bases) to CS probe (2) forms a double stranded promoter, made complete by the three bases (8) in target (6), and therefore a split promoter is formed to yield a *de novo* synthesised RNA (14) in the presence of T7 RNA polymerase.

The *de novo* synthesised RNA species is then amplified, as represented in Figure 13. Referring to Figure 13, RNA molecule (14) contains an overlap sequence, a second promoter sequence (SP6, designated as Pr (2) in Figures 12 and 13) and a further 6 bases to compensate for possible early termination of transcription. This molecule (14) anneals to added DNA probe 3 (50 in Figure 13) in the amplification scheme, creating a double stranded SP6 promoter and thus initiates the amplification cycle (step i). The RNA transcript (52) from probe 3 (50) includes a different overlap sequence to that of RNA molecule (14), a sequence for T3 RNA polymerase promoter (promoter 3 or Pr 3) and a further 6 bases. This molecule (52) anneals (step ii) to added DNA probe 4, (54 in Figure 13) creating a double stranded T3 promoter which initiates the transcription (step iii) of RNA (56) anneals (step iv) to probe 3 (50) in a continuation of the amplification cycle. Note that promoters 1, 2 and 3 need not be necessarily T7, SP6 and T3 RNA polymerase

promoters respectively: they could be used in a different order to that shown, or one or more other RNA promoters not discussed here may alternatively be employed.

In contrast to the amplification system illustrated in Figure 3, an active RNA promoter is formed directly by hybridisation of appropriate nucleic acid sequences in the system described above, there is no extension required for promoter formation.

7.1 Preparation of Oligonucleotides

The target oligonucleotides and probes are synthesised and purified as described in Example 1.

7.2 RNA synthesis by split promoter and amplification cycle

Hybridisation reactions comprise mixtures of DNA including target oligonucleotide, PS and CS probes, probe 3 and probe 4 together with relevant controls comprising mixtures with and without target/PS or CS probes and probes 3 and 4. For hybridisation reactions, 40 fmol of target oligonucleotide is mixed with 40 fmol each of probes PS, CS, 3 and 4 in a solution containing 4 μ l 5 x RNA polymerase buffer (giving 1 x concentrations of 40mM Tris (pH7.9), 6 mM $MgCl_2$, 2 mM spermidine and 10 mM NaCl) and distilled water to a final volume of 20 μ l (following final addition of T7, SP6 and T3 RNA polymerases and rNTP mix). The mixture is heated to 90°C for 3 minutes to denature the nucleic acids, incubated on ice for 2 minutes, and equilibrated to 37°C for 1 minute. Probes are annealed and transcribed at 37°C for 180 minutes by addition of 40 units of each RNA polymerase (Promega) and 120 nmoles of each rNTP (Pharmacia Biotech). DNA oligonucleotides are removed from the reaction mix by heating to 90°C for 3 minutes and incubating on ice for 2 minutes followed by the addition of 4 units of DNase I (Ambion) and incubating at 37°C for 20 minutes prior to end detection. One (or potentially both) of the resulting products (RNAs 14 & 52) may be detected by the hybridisation of molecular beacon (see below).

7.3 Detection of RNA by Molecular Beacon Assay

5 μ l of reaction sample was added to the reaction mix consisting of 145 μ l of hybridisation solution and 2 pmol molecular beacon (5' fluorophore = FAM; 3' quencher = methyl red

probe 5), in a Labsystems White Microstrip well plate, which is incubated in the dark at room temperature for 60 minutes. Fluorescence signal from the hybridised beacon/target is measured using the Wallac Victor 1420 Multilabel Counter, using the fluorescein protocol.

7.4 List of oligonucleotides

Target oligonucleotide (Normal wild type CFTR DNA)

5' TTATGCCTGGCACCATTAAAGAAAATATCATCttGGTGTTCCTATGATGA
ATATAGATACAGAAGCGTCATCAAAGC 3' (Seq. ID No. 16)

CS probe (T7 promoter)

5' ATAGGAAACACCAAAGATGATATTTTCTTTAATACGACTCACTATA 3' (Seq.
ID No. 17)

PS Probe (T7 promoter (Pr1) with 3' ATT 5' start sequence in target, and template
portion which encodes transcript with SP6 promoter (Pr2))

SP6 promoter T7 promoter
5' GTATTCTATAGTGTACCTAAATATTTACGCGATAAGTATCTCCCTATAGT
GAGTCGTA 3' (Seq. ID No. 38)

Probe 3 (first DNA oligo in amplification cycle with SP6 promoter (Pr2), encoding
transcript with T3 promoter (Pr3))

T3 promoter molecular
5' CTTCCCTTTAGTGAGGGTTAATAATGCCTCCTTGTCTCCGTTCTCGTGGAAT
beacon sequence SP6 promoter
GTTGCCACACCTAGTGCCACGTATTCTATAGTGTACCTAAATATTTACGCGAT
3' (Seq. ID No. 39)

Probe 4 (second DNA oligo in amplification cycle with T3 promoter (Pr3) encoding
transcript with SP6 promoter (Pr2))

SP6 promoter molecular
5' GTATTCTATAGTGTACCTAAATATTTACGCGATAAGTACGTGGAATGTTG
beacon sequence T3 promoter
CCCACACCTAGTGCCACCTTCCCTTTAGTGAGGGTTAATAATGCCTCCTTGTCTCC

3' (Seq. ID No. 40)

Probe 5 (molecular beacon: 5' fluorescent label and 3' quencher)

FAM 5' CGCGCGTGGAATGTTGCCCCACACCTAGTGCCCACCGCG 3' Methyl red
(Seq. ID No. 41)

Example 8: Transcription from a split T7 RNA Pol promoter 2½ way junction, using an RNA target

This example involves the use of an RNA target (based on the CFTR sequence). The complete T7 promoter is located towards the 3' end of CS probe. The first three (5') bases of the promoter sequence is complemented by three bases (3'AUU 5') in the target, when CS probe hybridises to the target. Hybridisation of a second oligonucleotide (PS probe, at the 3' end of which is the complement to the T7 promoter minus three bases) to CS probe forms a double stranded promoter, made complete by the three bases in the target, and therefore a split promoter is formed to yield a *de novo* synthesised RNA in the presence of T7 RNA polymerase. This reaction was compared to a control reaction which used a DNA version of the CFTR target. This example shows that sample RNA could be used as a target for the split promoter (i.e. that the polymerase will recognise a promoter which comprises at least three bases of RNA rather than DNA). Furthermore, the resulting RNA transcript could be further amplified using a second split promoter. The RNA signal from this second promoter could be again amplified by re-forming the previous split promoter, and so on, in an amplification cycle relying on the presence of T7 RNA polymerase and rNTPs only (e.g. as illustrated schematically in Figure 15).

8.1 Preparation of oligonucleotides

The target oligonucleotides and probes were synthesised and purified as described in example 1.

8.2a Synthesis and quantification of RNA target

RNA target molecules were prepared by transcription with T7 RNA polymerase, under standard conditions, of a double stranded DNA oligonucleotide prepared so as to include a T7 polymerase promoter. DNA oligonucleotides were then removed from the reaction

mix by addition of 3 units of DNase I (Ambion) and incubation at 37°C for 10 minutes, followed by heat inactivation of the enzyme at 90°C for 3 minutes. The transcript was quantified using the RiboGreen RNA Quantitation Kit (Molecular Probes, R-11490).

For quantification, 5 µl of the reaction mixes, or of dilutions in TE were added to 95 µl of TE in the well of a Labsystems White Microstrip well plate, together with 100 µl of the Quantitation Reagent (a 1/2000 dilution of the Quantitation Reagent in TE, according to the manufacturer's instructions). The plate was shaken at 200 rpm for 5 minutes at 22°C, followed by detection of fluorescence signal from the intercalated fluorophore/RNA measured using the Wallac Victor 1420 Multilabel Counter, using the fluorescein protocol. The fluorescence signal value was converted to pmol RNA by comparison to a standard curve measured in the same way as the transcript, but using a standard synthetic RNA (probe 3, below). The quantified RNA was stored in 10 µl aliquots at -80°C.

8.2b Split promoter probe and RNA synthesis

Hybridisation reactions comprised mixtures of DNA including target RNA or DNA oligonucleotide, CS probe and PS probe together with relevant controls comprising mixtures with and without target/probes CS and PS. For hybridisation reactions, 50 fmol of target RNA or DNA oligonucleotide was mixed with 50 fmol of CS probe and 50 fmol of PS probe in a solution containing 28.3 µl T7 RNA polymerase buffer (giving 1x concentrations of 40mM Tris (pH8.1), 20 mM MgCl₂, 1 mM spermidine, 5 mM DTT (Promega P117C), 80mg/ml PEG 8000, 50 µg/ml BSA, and 0.01% Triton X-100: Milligan *et al.*, 1987, Nucleic Acids Research, volume 15, pp. 8783-8798) and distilled water to a final volume of 50 µl (following final addition of T7 RNA polymerase and rNTP mix). The mixture was heated to 90°C for 3 minutes to denature the nucleic acids, then cooled to 10°C at 0.1°C per second for hybridisation. Probes were annealed and transcribed at 37°C for 180 minutes by addition of 25 units of T7 RNA polymerase and 40 nmoles of each rNTP. DNA oligonucleotides were removed from the reaction mix by the addition of 3 units of DNase I and incubating at 37°C for 10 minutes, followed by heating to 90°C for 3 minutes, and cooling to 15°C, prior to end detection. The resulting product was immobilised by hybridisation to a specific biotinylated oligonucleotide (probe 4, below) which was in turn bound to a streptavidin coated well. The immobilised product

was detected by colorimetry via the hybridisation of probe 5 (see below), an alkaline phosphatase-labelled oligonucleotide probe.

8.3 Detection of RNA by Colorimetry

5 μ l of reaction sample or dilutions was added to the reaction mix consisting of 145 μ l hybridisation buffer (20 mM EDTA pH 8.0, 1 M NaCl, 50 mM Tris, 0.1% bovine serum albumin, mixture adjusted to pH 8.0 with HCl), 0.9 pmol of probe 4 and 6 pmol of probe 5 in a Labsystems streptavidin coated well plate, which was incubated at 22°C for 60 minutes. Unbound material was removed by washing the wells 4x with 200 μ l of wash solution (0.25 M Tris, 0.69 M NaCl, 13.4 mM KCl, adjusted to pH 8.0 with HCl), and 1x with substrate buffer (used as a 1x solution, made from a 5x concentrate stock obtained from Boehringer Mannheim). 180 μ l of substrate buffer containing 5 mg/ml of 4-nitrophenyl phosphate was added to the well, and colour development was measured by optical density at 405 nm using a Labsystems integrated EIA Management system plate reader, readings taken every 2 minutes for 30 minutes. Results are shown in Figure 14.

Figure 14 is a bar chart showing the amount of RNA produced (in picomoles) using either an RNA target (left hand columns) or a DNA target (right hand columns). For each group of columns, (1) gives the results obtained for mixtures comprising target and first and second probes; (2) gives the results obtained in the absence of target; and (3) gives the results obtained in the absence of target and first probe.

It can be seen that, although a DNA target results in the production of more RNA, both DNA and RNA targets can be used successfully to form functional "split" promoters. In either case the background signal is very low.

8.4 List of oligonucleotides

RNA target (sequence based on normal wild type CFTR DNA) (Seq. ID No. 42)

5'GGGAGAUGAUGACGCUUCUGUAUCUAUAUUCUAUCAUAGGAAACACCAAA
GAUGAUUUUUUCUUUAUGGUGCCAGGCAUAAUCCAGGAAAACUGAGAACA3'

DNA target oligonucleotide (Normal wild type CFTR DNA)

5'GTTGGCATGCTTTGATGACGCTTCTGTATCTATATTCATCATAGGAAACACC
AAAGATGATATTTTCTTTAATGGTGCCAGGCATAATCCAGGAAAAGTCTGAGAA
CAGAATGAAATTCTTC3' (Seq. ID No. 32)

CS probe (T7 promoter with complementary 3'ATT5' start sequence in target)

5'CAGTTTTCTGGATTATGCCTGGCACCATTAAATACGACTCACTATA3'
(Seq. ID No. 35)

PS probe (T7 promoter and template)

5'TGCCTCCTTGTCTCCGTTCTGGATATCACCCGATGTGTCTCCCTATAGTGAG
TCGTA3' (Seq. ID No. 19)

Probe 3 (RNA control for constructing the standard curve in the RiboGreen assay)

5'GGGAGACACAUCGGGUGAUUAUCCAGAACGGAGACAAGG3' (Seq. ID No. 43)

Probe 4 (with 5' biotin to allow capture on streptavidin coated plates)

5'TCCGCTGCCTCCTTGTCTCCGTTCT3' (Seq. ID No. 21)

Probe 5 (alkaline phosphatase-labelled)

5'GGATATCACCCG3' (Seq. ID No. 22)

Example 9: Transcription of a ribozyme from a split T7 RNA Pol promoter at a 2½ way junction

In this example RNA produced from a split promoter has the sequence of a known ribozyme (Clouet-D'Orval & Uhlenbeck, 1996 RNA 2(5): 483-491) and can bind to a dual labelled single stranded oligonucleotide to form a functional ribozyme. Cleavage of the labelled oligonucleotide at a specific site will then generate a signal. The complete T7 promoter is located towards the 3' end of CS probe. The first three (5') bases of the promoter sequence is complemented by three bases (3'ATT 5') in the target, when CS probe hybridises to the target. Hybridisation of a second oligonucleotide (PS probe, at the 3' end of which is the complement to the T7 promoter minus three bases) to CS probe

forms a double stranded promoter, made complete by the three bases in the target, and therefore a split promoter is formed to yield a *de novo* synthesised RNA ribozyme in the presence of T7 RNA polymerase.

9.1 Preparation of oligonucleotides

The target oligonucleotides and probes are synthesised and purified as described in example 1.

9.2 Split promoter probe and RNA synthesis

Hybridisation reactions comprise mixtures of DNA including target oligonucleotide, CS probe and PS probe together with relevant controls comprising mixtures with and without target/probes CS and PS. For hybridisation reactions, 40 fmol of target oligonucleotide is mixed with 40 fmol of CS probe and 40 fmol of PS probe in a solution containing 4 μ l 5x T7 RNA polymerase buffer (giving 1x concentrations of 40mM Tris (pH7.9), 6 mM $MgCl_2$, 2 mM spermidine and 10 mM NaCl) and distilled water to a final volume of 20 μ l (following final addition of T7 RNA polymerase and rNTP mix). The mixture is heated to 90°C for 3 minutes to denature the nucleic acids, then cooled to 10°C at 0.1°C per second for hybridisation. Probes are annealed and transcribed at 37°C for 180 minutes by addition of 40 units of T7 RNA polymerase and 40 nmoles of each rNTP. DNA oligonucleotides are removed from the reaction mix by the addition of 3 units of DNase I and incubating at 37°C for 20 minutes prior to end detection.

9.3 Detection of synthesised RNA

5 μ l aliquots of sample or 5 μ l of a suitable dilution of the treated assay sample are added to 100 μ l buffer (50 mM Tris-HCl pH7.5, 20 mM $MgCl_2$, 10 % ethanol), followed by 10 pmol probe 3. This double-labelled RNA (5'-Tamra, 3'-Fam) is the ribozyme substrate. The RNA product of the 2½ way junction (formed in the presence of specific target) is designed to be the corresponding "hammerhead" ribozyme. Probe 3 therefore anneals to the RNA product, creating a functional ribozyme. Ribozyme cleavage of the substrate, which results in the removal of the quencher from the fluorophore, can be monitored by Fluorescence Resonance Energy Transfer (Tamra excitation at 546 nm, emission at 579 nm). Alternatively, substrate cleavage could be measured by a decrease

in fluorescence polarisation. Since substrate turnover is possible, a level of amplification may be achieved during the detection process.

Alternative real time detection system

Real time detection would be possible if the ribozyme substrate molecule is included in the extension / transcription reaction mixture, under suitable buffer conditions.

Alternative detection systems:

The RNA product could include a capture sequence, allowing it to be captured on to a streptavidin-coated well via a biotinylated capture probe. After wash steps to remove unbound material, probe 3 could be added and ribozyme cleavage could be monitored as described above.

Alternative labels could be attached to the ribozyme substrate molecule.

9.4 List of oligonucleotides

Target oligonucleotide (Normal wild type CFTR DNA)

5'GTTGGCATGCTTTGATGACGCTTCTGTATCTATATTCATCATAGGAAACACC
aaaGATGATATTTTCTTTAATGGTGCCAGGCATAATCCAGGAAAACCTGAGAACA
GAATGAAATTCTTC3' (Seq. ID No. 32)

CS probe (T7 promoter with 3'ATT5' start sequence in target)

5'CAGTTTTCTGGATTATGCCTGGCACCATTAAATACGACTCACTATA3'
(Seq. ID No. 35)

PS probe (T7 promoter and template, which encodes the ribozyme)

5'GAATCTCATCAGTAGCGAGTTCTCTCTCCCTATAGTGAGTCGTA3'
(Seq. ID No. 44)

Probe 3 (ribozyme substrate)

5'Tamra-GAAUCGAAACGCGAAAGCGUCUAGCGU-FAM3'

(Seq. ID No. 45)

Example 10:

An experiment was conducted to determine the optimum sequence of +12 region for most efficient transcription by T7 RNA polymerase.

Accordingly a series of second probe molecules were prepared, each comprising identical T7 promoter, detection and capture sequences but having different +12 sequences adjacent to the T7 promoter sequence. These probes were hybridised to a complementary 22 base oligonucleotide (containing the complementary strand of the T7 promoter) under identical conditions, and the amount of RNA produced was determined as described in the previous examples.

Table 2 below shows the relative "RNA transcription factor" for each of the different +12 sequences tested.

Table 2. Alternative template T7 +1 to +12 sequences in descending order of transcription efficiency.

+1 to +12 sequence	RNA transcription factor
5' GTTCTCTCTCCC 3'	142
5' GCTCTCTCTCCC 3'	115
5' GTTGTGTCTCCC 3'	110
5' GATGTGTCTCCC 3'	105
5' ATCCTCTCTCCC 3'	96
5' GTTCTCGTGCCC 3'	84
5' ATCCTCGTGCCC 3'	76
5' GCTCTCGTGCCC 3'	64
5' GTTGTGGTGCCC 3'	21

Claims

1. A method of detecting the presence of a nucleic acid target sequence of interest, the method comprising the steps of:
 - (a) adding first and second nucleic acid probes to a sample comprising the sequence of interest, so as to form a complex comprising three strands of nucleic acid, wherein the first probe comprises the full length sequence of a first strand of a double stranded promoter, the target sequence comprises an end part of a second strand of the double stranded promoter which is complementary to a part of the first strand, and the second probe comprises the rest of the second strand of the double stranded promoter which is complementary to a part of the first strand, such that a functional promoter is formed when the first probe is hybridised to both the target sequence and to the second probe;
 - (b) adding a polymerase which recognises the promoter, so as to cause the *de novo* synthesis of nucleic acid from the promoter present in the complex; and
 - (c) detecting directly or indirectly the *de novo* synthesised nucleic acid.
2. A method according to claim 1, wherein the promoter is an RNA polymerase promoter and the *de novo* synthesised nucleic acid is RNA.
3. A method according to claim 1 or 2, wherein the promoter is recognised by T3, T7 or SP6 RNA polymerase or a mutant form thereof.
4. A method according to any one of the preceding claims, wherein the second probe comprises a template portion which may act as a template for synthesis of nucleic acid from the functional promoter.
5. A method according to claim 4, wherein the second probe comprises a +12 region adjacent to the promoter to optimise transcription from the promoter.

6. A method according to claim 5, wherein the second probe comprises a +12 region sequence selected from the group consisting of:

(5'→3') GTTCTCTCTCCC; GCTCTCTCTCCC; GTTGTGTCTCTCCC; GATGTGTCTCTCCC; ATCCTCTCTCTCCC; GTTCTCGTGCCCC; ATCCTCGTGCCCC; GCTCTCGTGCCCC; and GTTGTGGTGCCCC.

7. A method according to any one of claims 4, 5 or 6, wherein the template portion, when copied by the polymerase, provides a sequence which can act as an RNA polymerase promoter, or may be used for detection and/or capture at a solid surface.

8. A method according to any one of claims 4-7, wherein the template portion, when copied by the polymerase, provides a sequence which hybridises with a molecular beacon.

9. A method according to any one of claims 4-7, wherein the template portion, when copied by the polymerase, provides a sequence which acts as a ribozyme.

10. A method according to any one of the preceding claims, wherein the *de novo* synthesised nucleic acid is subjected to an amplification step prior to detection.

11. A method according to claim 10, wherein the amplification step comprises: hybridising the *de novo* synthesised nucleic acid to a third nucleic acid probe, which hybridisation forms a second double stranded nucleic acid promoter either directly, or by 3' extension of the *de novo* synthesised nucleic acid using the third probe as template; and adding a polymerase which recognises the second promoter so as to cause nucleic acid synthesis therefrom.

12. A method according to claim 10, wherein the nucleic acid synthesised from the second promoter is detected.

13. A method according to claim 11, further comprising the steps of: hybridising the nucleic acid synthesised from the second promoter to a fourth nucleic acid probe, which

hybridisation forms a third double stranded nucleic acid promoter either directly, or by 3' extension of the nucleic acid synthesised from the second promoter using the fourth probe as template; and adding a polymerase which recognises the third promoter so as to cause nucleic acid synthesis therefrom.

14. A method according to claim 13, wherein nucleic acid synthesised from the third promoter is detected.

15. A method according to claim 13, further comprising the step of hybridising nucleic acid synthesised from the third promoter to the third probe, thereby reforming the second double stranded promoter, so as to create a cycle of nucleic acid synthesis.

16. A method according to claim 10, wherein the amplification step comprises: adding third and fourth nucleic acid probes so as to form a complex comprising the said probes and the *de novo* synthesised nucleic acid, wherein the third probe comprises the full length sequence of a first strand of a double stranded promoter, the *de novo* synthesised nucleic acid comprises an end part of a second strand of the double stranded promoter which is complementary to a part of the first strand, and the fourth probe comprises the rest of the second strand of the double stranded promoter which is complementary to a part of the first strand, such that a functional promoter is formed when the third probe is hybridised to both the *de novo* synthesised nucleic acid and to the fourth probe; adding a polymerase which recognises the promoter, so as to cause the synthesis of nucleic acid from the promoter present in the complex; and detecting directly or indirectly the synthesised nucleic acid.

17. A nucleic acid complex comprising three strands of nucleic acid: a promoter strand, a promoter complementary strand, and a target strand; wherein the promoter complementary strand comprises the full length sequence of a first strand of a double stranded promoter; the target strand comprises a part of a second strand of the double stranded promoter which is complementary to a part of the first strand; and the promoter strand comprises a part of the second strand of the double stranded promoter which is complementary to a part of the first strand; wherein neither part of the second strand of

the double stranded promoter present on the target strand or on the promoter strand is capable of forming a functional promoter when hybridised to the promoter complementary strand in the absence of the other part, but wherein a functional promoter is formed when the promoter complementary strand is hybridised to both the target strand and the promoter strand.

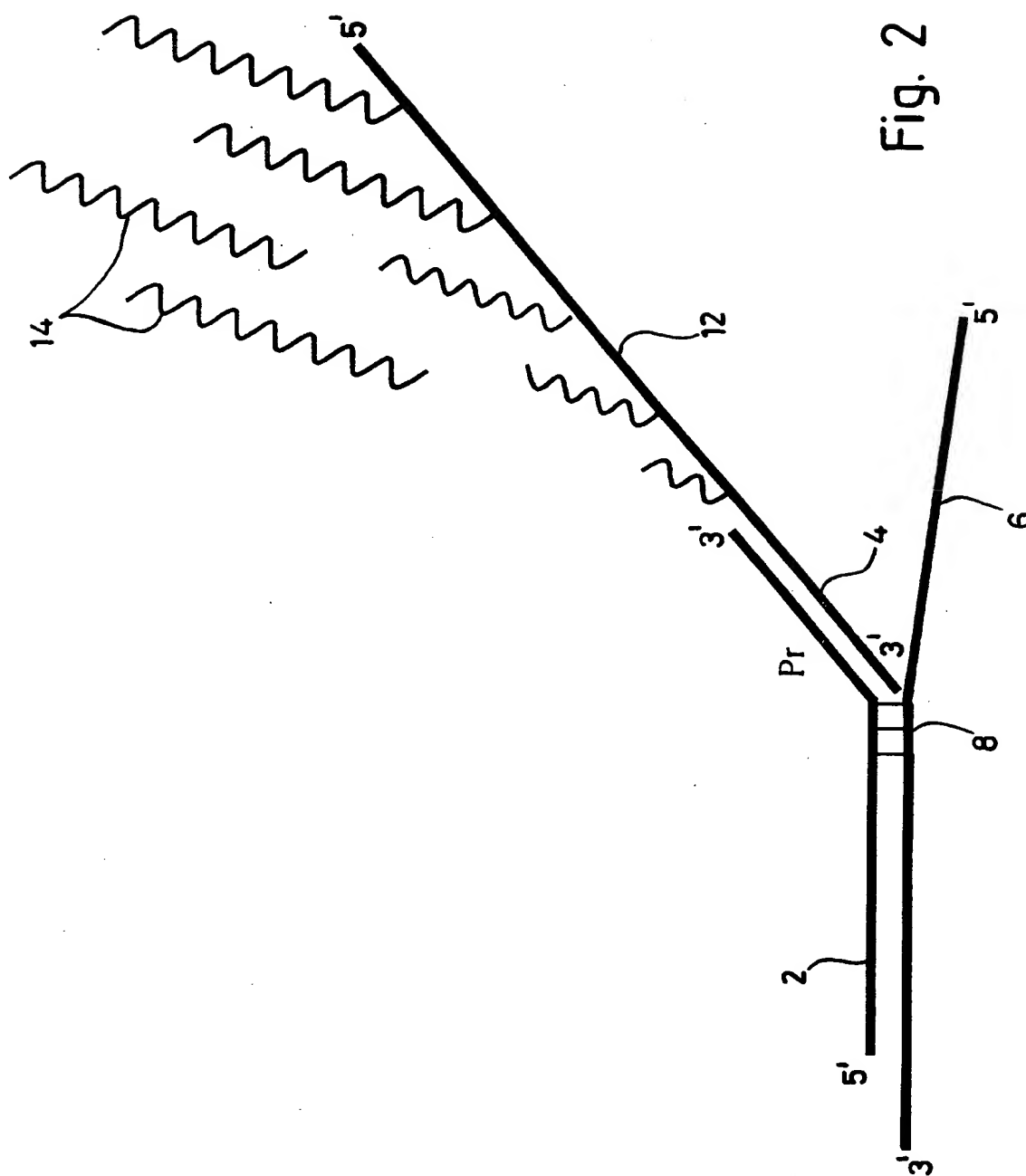
18. A complex according to claim 17, wherein the promoter complementary strand and promoter strand are provided by first and second nucleic acid probes respectively, the complex being formed in performance of a method according to any one of claims 1-16.

19. A kit for performing the method of claim 1, the kit comprising first and second probes for forming, together with the appropriate target sequence, the complex of claim 17, and instructions for performing the method of any one of claims 1-16.

20. A kit according to claim 19, further comprising one or more of the following: DNA polymerase; RNA polymerase; ribo- or deoxyribonucleotide triphosphates; labelling reagents; detection reagents; buffers.

21. A method substantially as hereinbefore described and with reference to the accompanying drawings.

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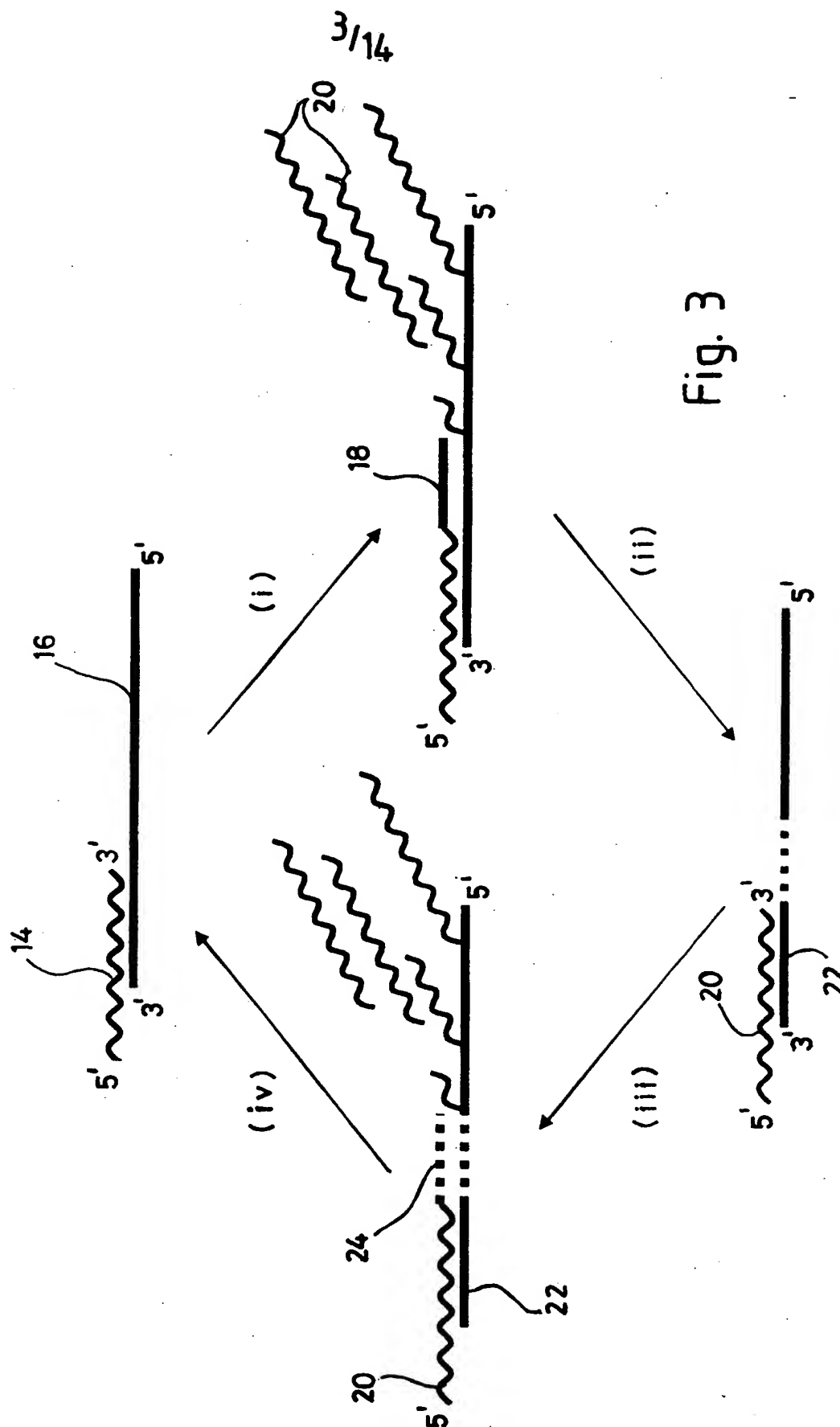


Fig. 3

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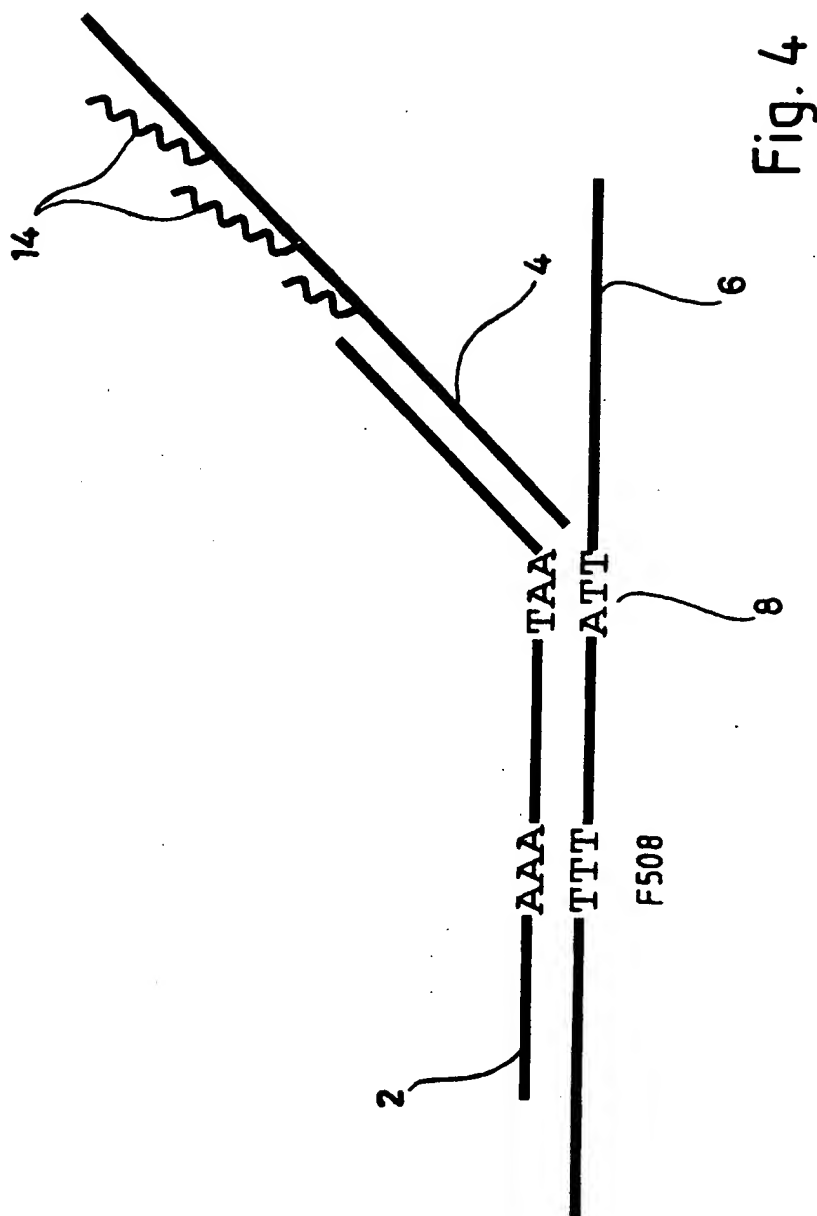


Fig. 4

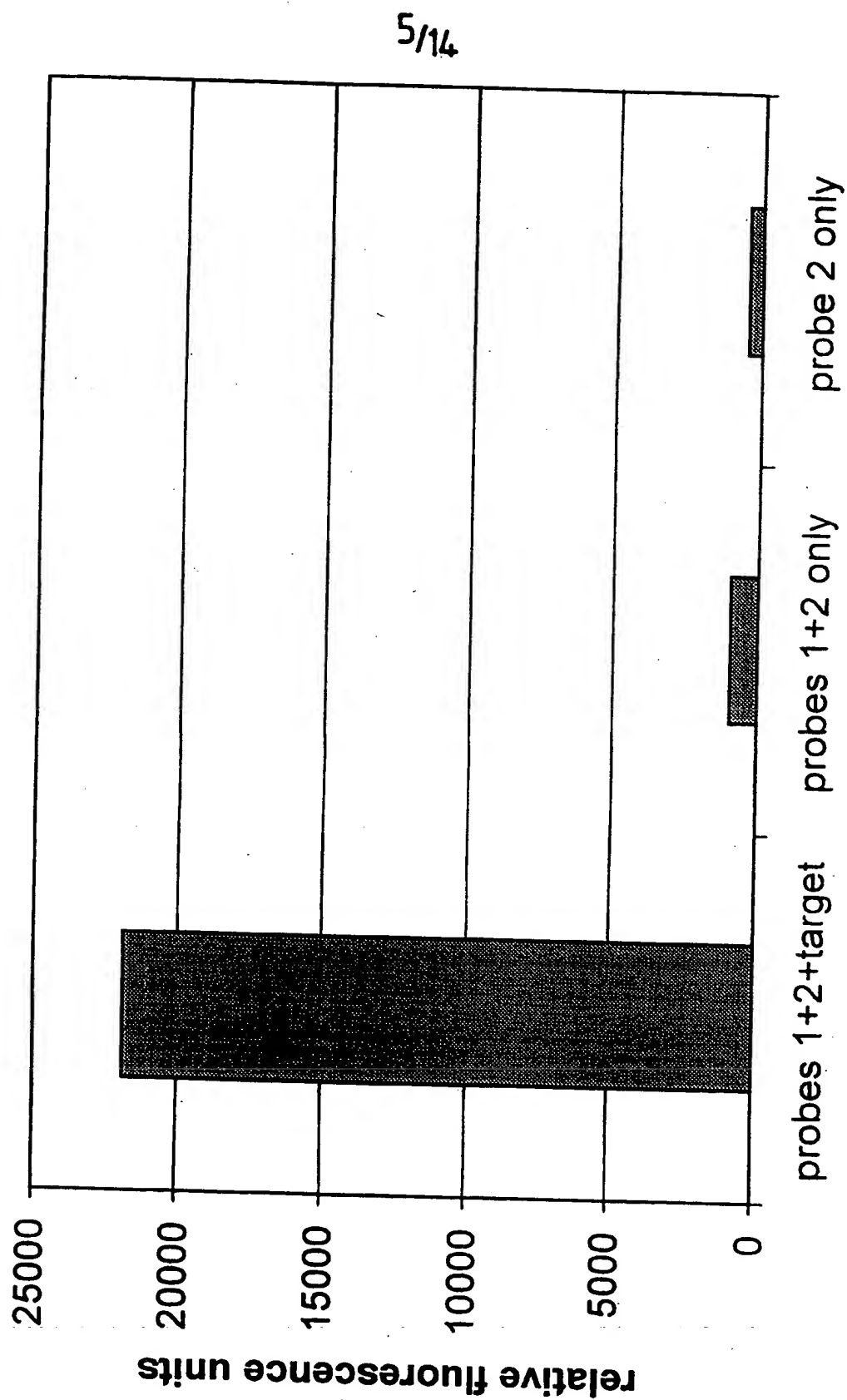
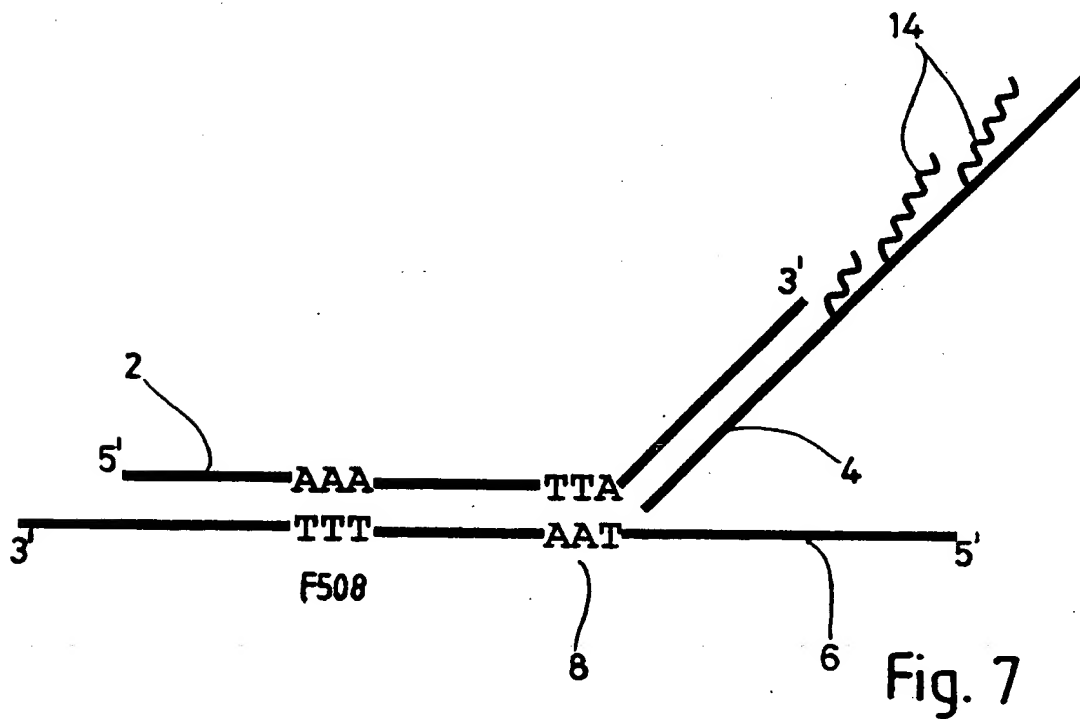
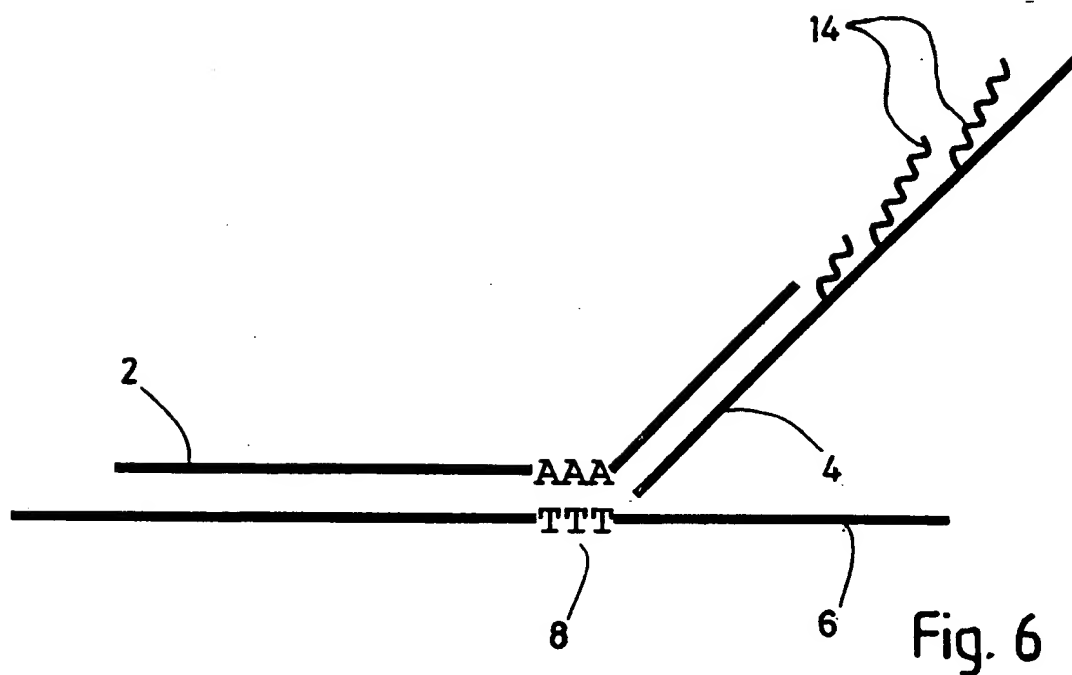
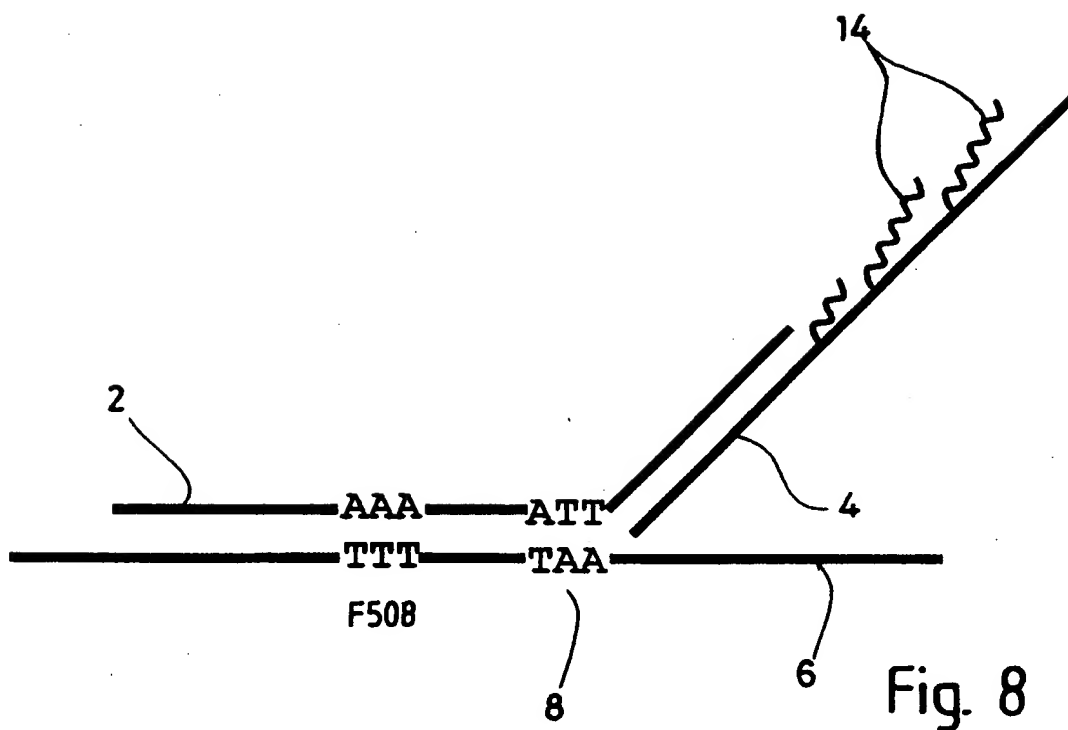


Fig. 5

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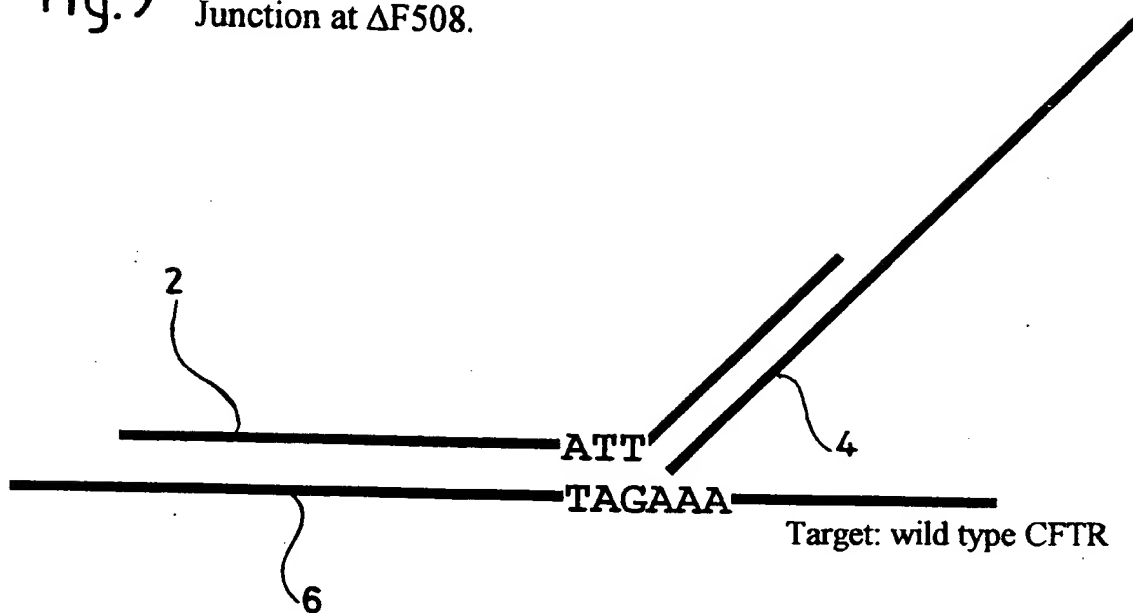


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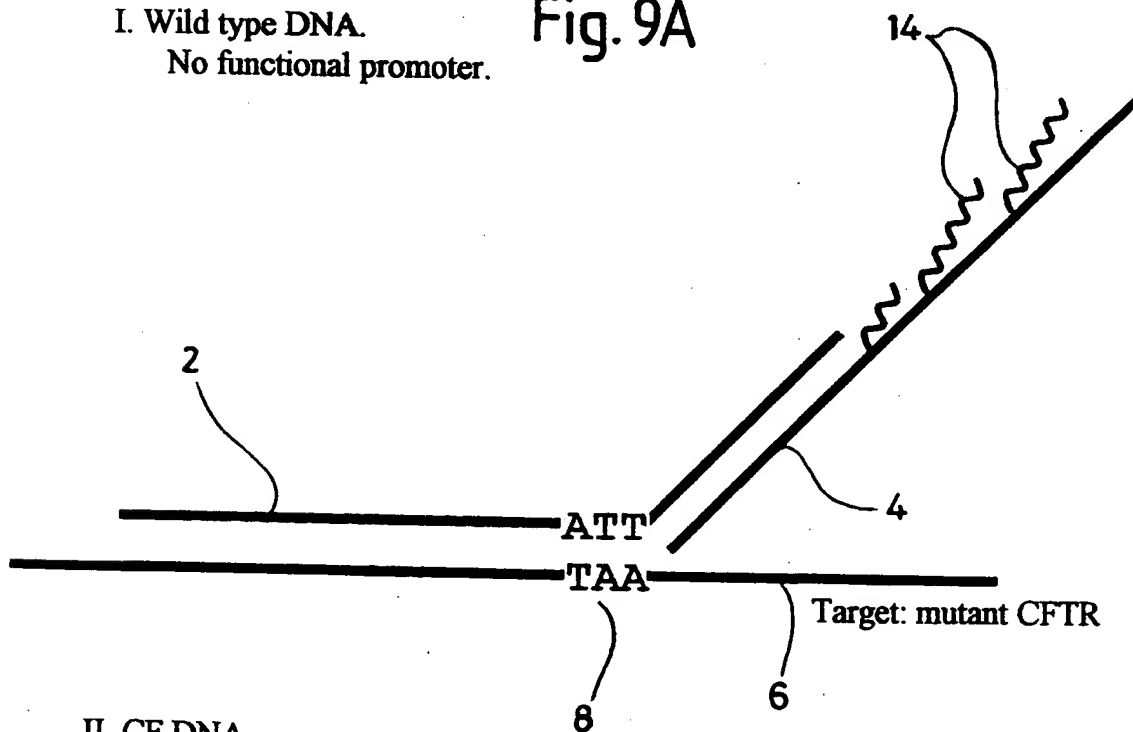


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Fig. 9 Transcription off a split SP6 RNA Pol promoter.
Junction at $\Delta F508$.



I. Wild type DNA.
No functional promoter.

Fig. 9A

II. CF DNA.
3bp of SP6 promoter formed
in target as a result of F508 mutation.

Fig. 9B

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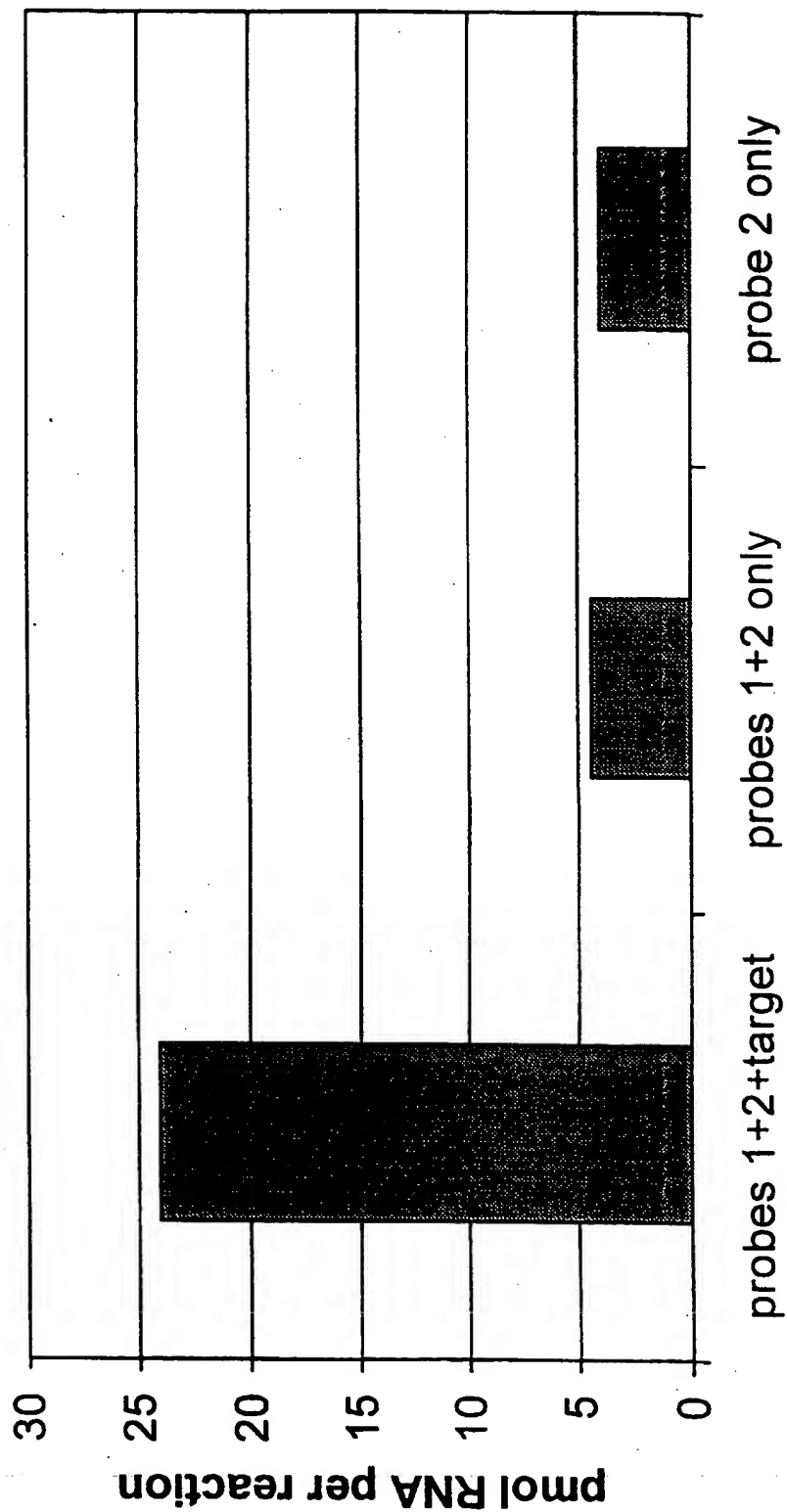


Fig. 10

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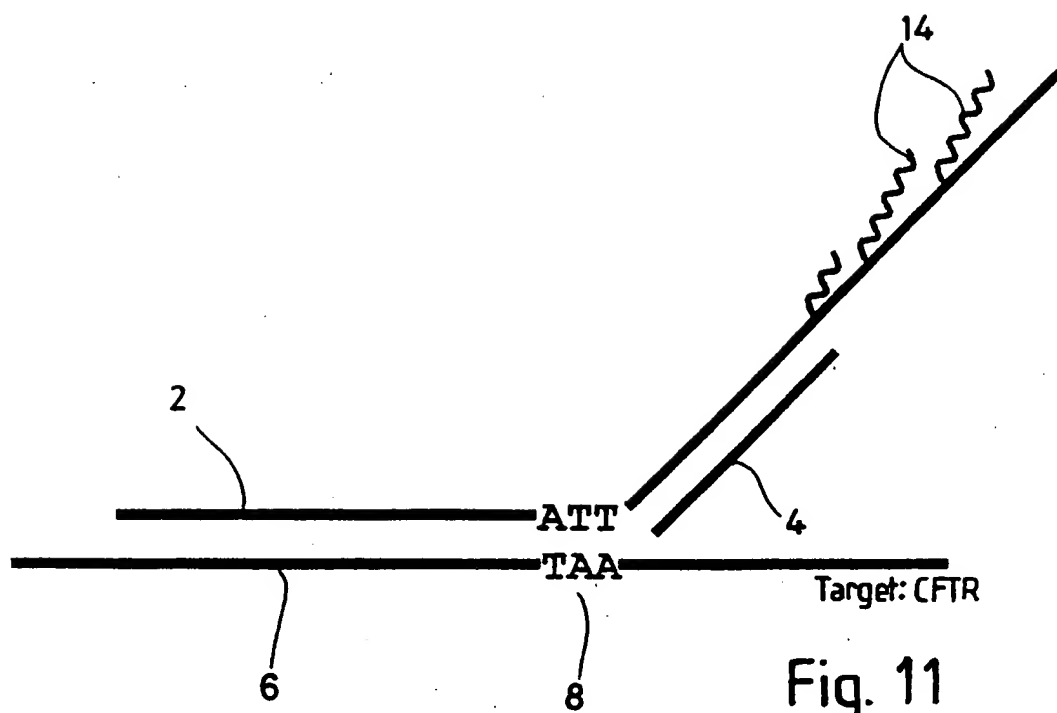


Fig. 11

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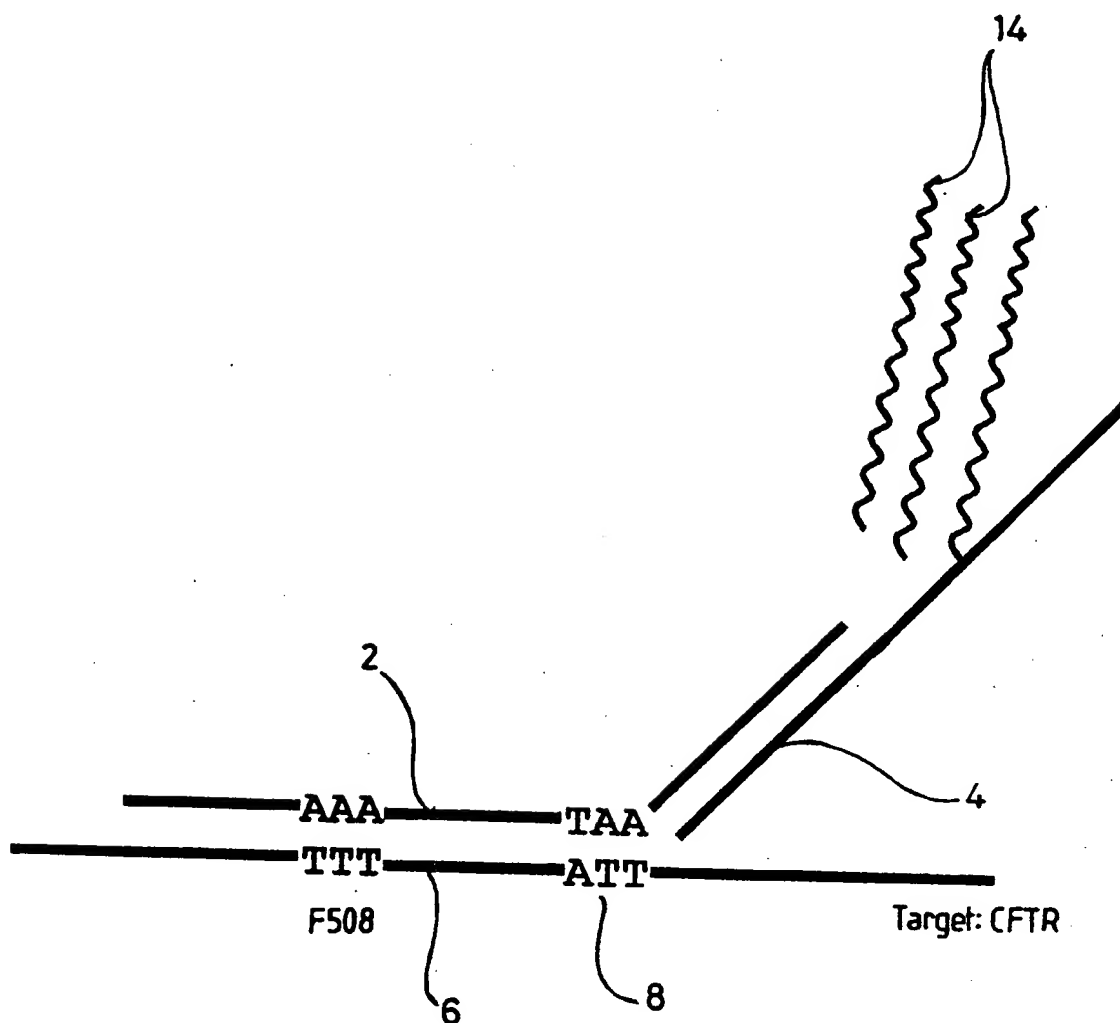


Fig. 12

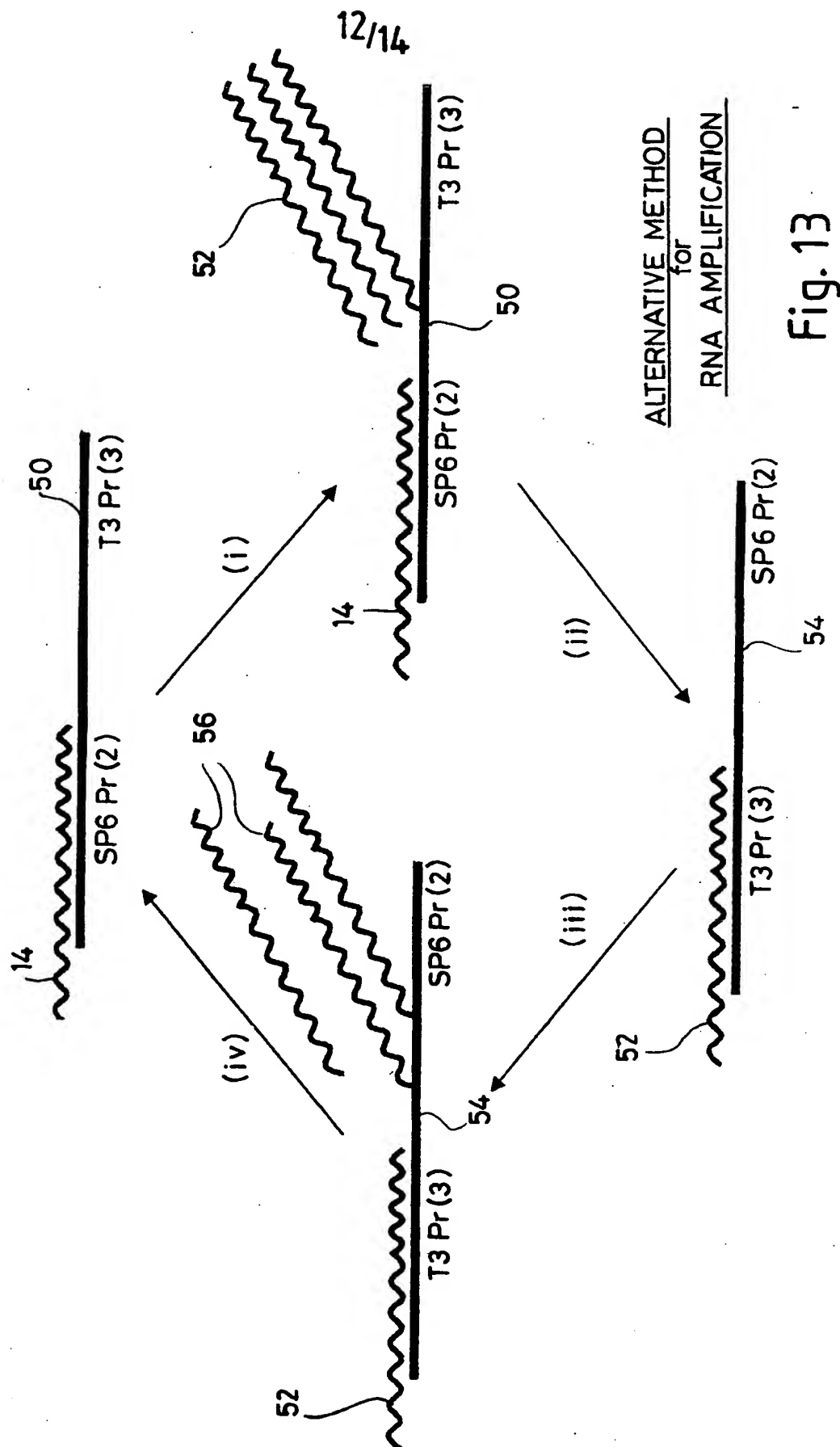


Fig. 13

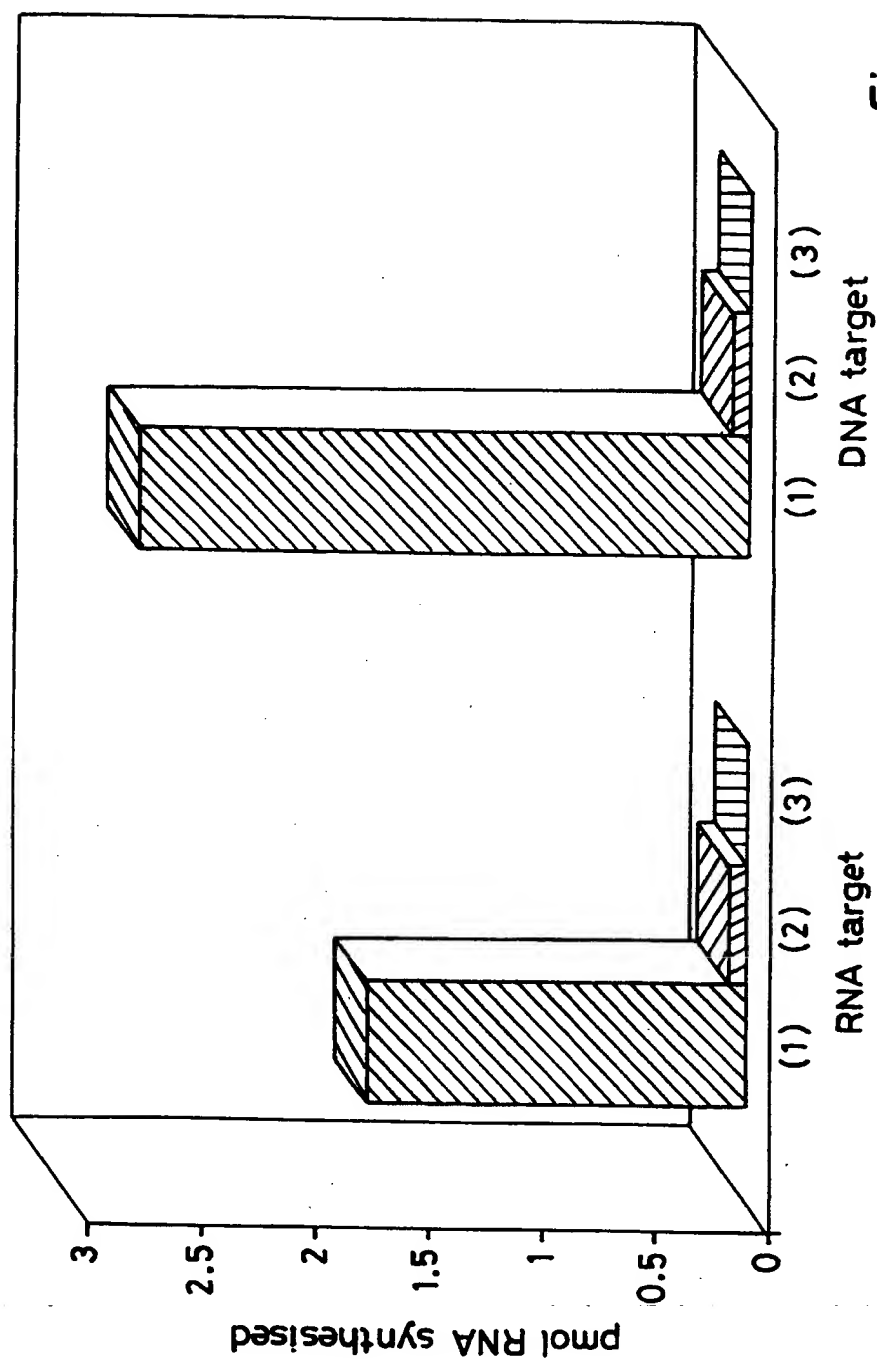


Fig. 14

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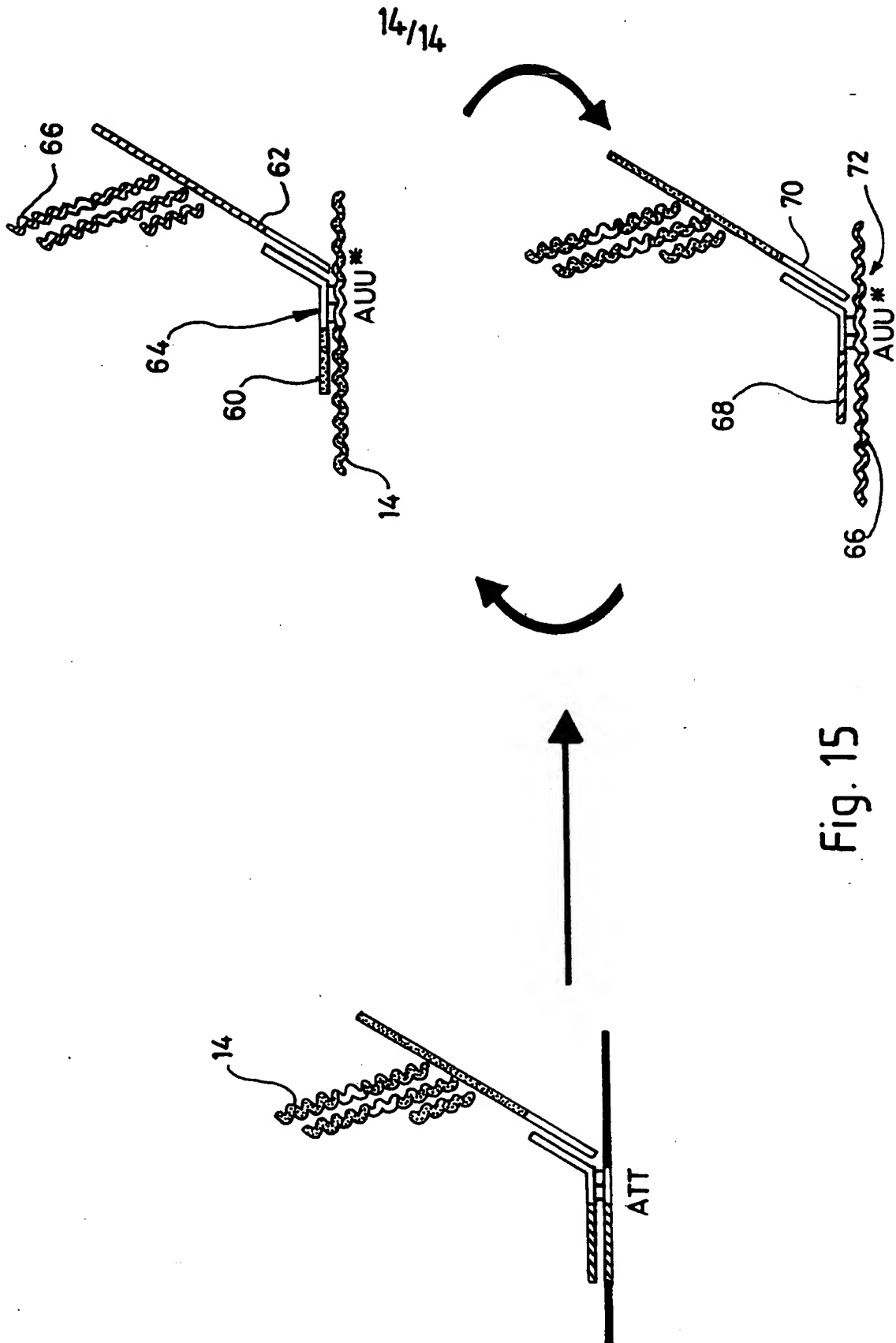


Fig. 15

1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Cytocell Limited
- (B) STREET: Unit 6, Somerville Court, Trinity Way
- (C) CITY: Adderbury, Banbury
- (E) COUNTRY: United Kingdom
- (F) POSTAL CODE (ZIP): OX17 3SN

(ii) TITLE OF INVENTION: Improvements in or Relating to Nucleic Acid Promoters

(iii) NUMBER OF SEQUENCES: 45

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAATTAACCC TCACTAAA

18

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TTTAGTGAGG GTTAATTT

18

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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TAATACGACT CACTATA

17

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TATAGTGAGT CGTATTA

17

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATTAGGTGA CACTATA

17

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TATAGTGTCA CCTAAAT

17

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTTCTCTCTC CC

12

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTCTCTCTC CC

12

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTTGTGTCTC CC

12

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
GATGTGTCTC CC 12
- (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
ATCCTCTCTC CC 12
- (2) INFORMATION FOR SEQ ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
GTTCTCGTGC CC 12
- (2) INFORMATION FOR SEQ ID NO: 13:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
ATCCTCGTGC CC 12
- (2) INFORMATION FOR SEQ ID NO: 14:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs

5

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GCTCTCGTGC CC

12

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTTGTGGTGC CC

12

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTATGCCTGG CACCATTAAA GAAAATATCA TCTTTGGTGT TTCCTATGAT GAATATAGAT

60

ACAGAAGCGT CATCAAAGC

79

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATAGGAAACA CCAAAGATGA TATTTTCTTT AATACGACTC ACTATA

46

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CCTTGTCTCC GTTCTGGATA TCACCCGATG TGTCTCCCTA TAGTGAGTCG TA 52

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCCTCCTTG TCTCCGTTCT GGATATCACC CGATGTGTCT CCCTATAGTG AGTCGTA 57

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TGCCTCCTTG TCTCCGTTCT 20

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCCGCTGCCT CTTGTCTCC GTTCT

25

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGATATCACC CG

12

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CTGTATCTAT ATTCATCATA GGAAACACCA AATTAACCCT CACTAAA

47

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCTTGTCTCC GTTCTGGATA TCACCCGATG TGATTCCCTT TAGTGAGGGT TAA

53

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GAGGCATAGC AGCAGGATGA AGAGGAAGAT GATAAACGC CGCAGACACA TCCAGCGATA 60
ACCAGGACAG GTTGGAGGAC AGGA 84

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TGGTTATCGC TGGATGTGTC TGCGGCGTTT TATTAACCCT CACTAAA 47

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTTCTATCCT GCACCGCCGG AGCTTTCAC CCCTCCCTT TAGTGAGGGT TAA 53

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CGCGATCCTG CACCGCCGGA GCTTTCACC CCGCG 35

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATTCATCATA GGAAACACCA AAGATGATAT TTAGGTGACA CTATA

45

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCTTGCTCTCC GTTCTGGATA TCACCCGATG TGGTATTCTA TAGTGTCACC TA

52

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GGATATCACC CG

12

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTTGGCATGC TTTGATGACG CTTCTGTATC TATATTCATC ATAGGAAACA CCAAAGATGA

60

10

TATTTTCTTT AATGGTGCCA GGCATAATCC AGGAAAAGT AGAACAGAAT GAAATTCTTC 120

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GTTGGCATGC TTTGATGACG CTTCTGTATC TATATTCATC ATAGGAAACA CCAATGATAT 60

TTTCTTTAAT GGTGCCAGGC ATAATCCAGG AAAACTGAGA ACAGAATGAA ATTCTTC 117

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTATGCCTGG CACCATTAAA GAAAATATCA TTTAGGTGAC ACTATA 46

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CAGTTTTCCT GGATTATGCC TGGCACCATT AATACGACTC ACTATA 46

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs

11

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CCTTGCTCC GTTCTGGATA TCACCCGATG TGTCTCCCTA TAGTGAGTCG TAAGAAAATA 60
TCATCTTTGG TGTTCCTAT GATG 84

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GGATATCACC CGATGTG 17

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GTATTCTATA GTGTCACCTA AATATTTTAC GCGATAAGTA TCTCCCTATA GTGAGTCGTA 60

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTTCCCTTTA GTGAGGGTTA ATAATGCCTC CTTGTCTCCG TTCTCGTGGA ATGTTGCCCA 60

CACCTAGTGC CCACGTATTC TATAGTGTC CCTAAATATT TCACGCGAT 109

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GTATTCTATA GTGTCACCTA AATATTTTAC GCGATAAGTA CGTGGAATGT TGCCACACCC 60
TAGTGCCAC CTTCCCTTTA GTGAGGGTTA ATAATGCCTC CTTGTCTCC 109

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CGCGCGTGGA ATGTTGCCCA CACCTAGTGC CCACGCGG 38

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GGGAGAUGAU GACGCUUCUG UAUCUAUAUU CAUCAUAGGA AACACCAAAG AUGAUUUUU 60
CUUUA AUGGU GCCAGGCAUA AUCCAGGAAA ACUGAGAACA 100

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:

13

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GGGAGACACA UCGGGUGAUA UCCAGAACGG AGACAAGG

38

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAATCTCATC AGTAGCGAGT TCTCTCTCCC TATAGTGAGT CGTA

44

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAAUCGAAAC GCGAAAGCGU CUAGCGU

27

INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 99/00265

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 93 06240 A (CYTOCELL LTD) 1 April 1993 cited in the application see claims 1-9; figures 1,2	1-21
A	EP 0 851 033 A (GEN PROBE INC) 1 July 1998 see figure 5	1-7
A	EP 0 552 931 A (GEN PROBE INC) 28 July 1993 see figure 15D	1-7
A	WO 94 29481 A (ASHER NATHAN) 22 December 1994	

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

29 June 1999

Date of mailing of the international search report

06/07/1999

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INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/GB 99/00265

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